

Sequence Listing

<110> Baker, Kevin
Botstein, David
Eaton, Dan
Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
Kljavin, Ivar
Napier, Mary
Roy, Margaret
Tumas, Daniel
Wood, William

<120> SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

<130> P2548P1C1

<150> 60/067,411

<151> December 3, 1997

<150> 60/069,334

<151> December 11, 1997

<150> 60/069335

<151> December 11, 1997

<150> 60/069,278

<151> December 11, 1997

<150> 60/069,425

<151> December 12, 1997

<150> 60/069,696

<151> December 16, 1997

<150> 60/069,694

<151> December 16, 1997

<150> 60/069,702

<151> December 16, 1997

<150> 60/069,870

<151> December 17, 1997

<150> 60/069,873

<151> December 17, 1997

<150> 60/068,017

<151> December 18, 1997

<150> 60/070,440

TO THE PCT/US98/25108

- <151> January 5, 1998
- <150> 60/074,086
<151> February 9, 1998
- <150> 60/074,092
<151> February 9, 1998
- <150> 60/075,945
<151> February 25, 1998
- <150> 60/112,850
<151> December 16, 1998
- <150> 60/113,296
<151> December 22, 1998
- <150> 60/146,222
<151> July 28, 1999
- <150> PCT/US98/19330
<151> September 16, 1998
- <150> PCT/US98/25108
<151> December 1, 1998
- <150> 09/216,021
<151> December 16, 1998
- <150> 09/218,517
<151> December 22, 1998
- <150> 09/254,311
<151> March 3, 1999
- <150> PCT/US99/12252
<151> June 22, 1999
- <150> PCT/US99/21090
<151> September 15, 1999
- <150> PCT/US99/28409
<151> November 30, 1999
- <150> PCT/US99/28313
<151> November 30, 1999
- <150> PCT/US99/28301
<151> December 1, 1999
- <150> PCT/US99/30095
<151> December 16, 1999
- <150> PCT/US00/03565
<151> February 11, 2000
- <150> PCT/US00/04414
<151> February 22, 2000

<150> PCT/US00/05841
<151> March 2, 2000

<150> PCT/US00/08439
<151> March 30, 2000

<150> PCT/US00/14042
<151> May 22, 2000

<150> PCT/US00/20710
<151> July 28, 2000

<150> PCT/US00/32678
<151> December 1, 2000

<150> PCT/US01/06520
<151> February 28, 2001

<160> 120

<210> 1
<211> 2454
<212> DNA
<213> Homo Sapien

<400> 1
ggactaatct gtgggagcag tttattccag tatcacccag ggtgcaggcca 50
caccaggact gtgttgaagg gtgtttttt tcttttaat gtaataaccc 100
ctcatctttt cttcttacac agtgtctgag aacatttaca ttatagataa 150
gtagtacatg gtggataact tctacttta ggaggactac tctcttcga 200
cagtcctaga ctggcttct acactaagac accatgaagg agtatgtgct 250
cctattatttc ctggcttctgt gctctgcaa acccttcttt agcccttcac 300
acatcgcaact gaagaatatg atgctgaagg atatggaaga cacagatgat 350
gatgatgatg atgatgatga tgatgatgat gatgaggaca actctctttt 400
tccaacaaga gagccaagaa gccattttt tccatttgat ctgtttccaa 450
tgtgtccatt tggatgtcag tgctattcac gagttgtaca ttgctcagat 500
ttaggtttga cctcagtcac aaccaacatt ccatttgata ctcgaatgct 550
tgatcttcaa aacaataaaa ttaaggaaat caaagaaaat gatttaaag 600
gactcaacttc actttatggc ctgatcctga acaacaacaa gctaacgaag 650
attcacccaa aagccttct aaccacaaag aagttgcgaa ggctgtatct 700
gtccccacaat caactaagtg aaataccact taatcttccc aaatcattag 750
cagaactcag aattcatgaa aataaagtta agaaaataca aaaggacaca 800

aaattgtctc ttcaaatacg tatggactgg ataactctga gaaacacatc 2300
tagtataact gaataagcag agcatcaa ataaacagaca gaaaccgaaa 2350
gctctatata aatgctcaga gttctttatg tatttcttat tggcattcaa 2400
catatgtaaa atcagaaaac agggaaattt tcattaaaaa tattggtttg 2450
aaat 2454

<210> 2
<211> 379
<212> PRT
<213> Homo Sapien

<400> 2
Met Lys Glu Tyr Val Leu Leu Leu Phe Leu Ala Leu Cys Ser Ala
1 5 10 15
Lys Pro Phe Phe Ser Pro Ser His Ile Ala Leu Lys Asn Met Met
20 25 30
Leu Lys Asp Met Glu Asp Thr Asp Asp Asp Asp Asp Asp Asp
35 40 45
Asp Asp Asp Asp Asp Glu Asp Asn Ser Leu Phe Pro Thr Arg Glu
50 55 60
Pro Arg Ser His Phe Phe Pro Phe Asp Leu Phe Pro Met Cys Pro
65 70 75
Phe Gly Cys Gln Cys Tyr Ser Arg Val Val His Cys Ser Asp Leu
80 85 90
Gly Leu Thr Ser Val Pro Thr Asn Ile Pro Phe Asp Thr Arg Met
95 100 105
Leu Asp Leu Gln Asn Asn Lys Ile Lys Glu Ile Lys Glu Asn Asp
110 115 120
Phe Lys Gly Leu Thr Ser Leu Tyr Gly Leu Ile Leu Asn Asn Asn
125 130 135
Lys Leu Thr Lys Ile His Pro Lys Ala Phe Leu Thr Thr Lys Lys
140 145 150
Leu Arg Arg Leu Tyr Leu Ser His Asn Gln Leu Ser Glu Ile Pro
155 160 165
Leu Asn Leu Pro Lys Ser Leu Ala Glu Leu Arg Ile His Glu Asn
170 175 180
Lys Val Lys Lys Ile Gln Lys Asp Thr Phe Lys Gly Met Asn Ala
185 190 195
Leu His Val Leu Glu Met Ser Ala Asn Pro Leu Asp Asn Asn Gly
200 205 210

TOPERSO "HOTEL 60

Ile Glu Pro Gly Ala Phe Glu Gly Val Thr Val Phe His Ile Arg
215 220 225

Ile Ala Glu Ala Lys Leu Thr Ser Val Pro Lys Gly Leu Pro Pro
230 235 240

Thr Leu Leu Glu Leu His Leu Asp Tyr Asn Lys Ile Ser Thr Val
245 250 255

Glu Leu Glu Asp Phe Lys Arg Tyr Lys Glu Leu Gln Arg Leu Gly
260 265 270

Leu Gly Asn Asn Lys Ile Thr Asp Ile Glu Asn Gly Ser Leu Ala
275 280 285

Asn Ile Pro Arg Val Arg Glu Ile His Leu Glu Asn Asn Lys Leu
290 295 300

Lys Lys Ile Pro Ser Gly Leu Pro Glu Leu Lys Tyr Leu Gln Ile
305 310 315

Ile Phe Leu His Ser Asn Ser Ile Ala Arg Val Gly Val Asn Asp
320 325 330

Phe Cys Pro Thr Val Pro Lys Met Lys Lys Ser Leu Tyr Ser Ala
335 340 345

Ile Ser Leu Phe Asn Asn Pro Val Lys Tyr Trp Glu Met Gln Pro
350 355 360

Ala Thr Phe Arg Cys Val Leu Ser Arg Met Ser Val Gln Leu Gly
365 370 375

Asn Phe Gly Met

<210> 3
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 3
ggaaatgagt gcaaaccctc 20

<210> 4
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 4
tcccaagctg aacactcatt ctgc 24

<210> 5
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 5
gggtgacggt gttccatatac agaattgcag aagcaaaact gacctcagtt 50

<210> 6
<211> 3441
<212> DNA
<213> Homo Sapien

<400> 6
cgacgcgtg ggccggacgcg tggggcccgs gcaccggccc cggcccgccc 50
ctccgccttc cgcaactcgcg cctccctccc tccgccccgt cccgcgcctt 100
cctccctccc tcctccccag ctgtccccgtt cgcgcatgc cgaggctccc 150
ggcccccggc gccccgtgc tgctccctcg gctgctgctg ctccggctccc 200
ggccggcccg cggccggcgc ccagagcccc ccgtgctgcc catccgttct 250
gagaaggagc cgctccccgt tcggggagcg gcaggctgca cttcggcgg 300
gaaggcttat gccttggacg agacgtggca cccggaccta gggcagccat 350
tcggggtgat gcgctgcgtg ctgtgcgcct gcgaggcgcc tcagtgggt 400
cgccgtacca gggccctgg cagggtcagc tgcaagaaca tcaaaccaga 450
gtgccccacc cccgcctgtg ggcagccgcg ccagctgccg ggacactgct 500
gccagacctg cccccaggag cgacgcgtt cggagcggca gccgagcggc 550
ctgtccctcg agtatccgcg ggaccggag catcgctgtt atagcgaccg 600
cggggagcca ggcgcgtgagg agcggggcccg tggtgacggc cacacggact 650
tcgtggcgct gctgacaggg ccgaggtcgc aggccgtggc acgagccga 700
gtctcgctgc tgcgctctag cctccgccttc tctatctcct acaggcgct 750
ggaccggccct accaggatcc gcttctcaga ctccaatggc agtgtccctgt 800
ttgagcaccc tgcagccccc acccaagatg gcctggcttg tggggtgtgg 850
cgggcagtgc ctcgggtgtc tctgcggctc ctttagggcag aacagctgca 900
tgtggcactt gtgacactca ctcacccttc aggggaggtc tgggggcctc 950
tcatccggca cccggccctg gctgcagaga cttcagtgc catcctgact 1000
ctagaaggcc ccccacagca gggcgttaggg ggcacacccc tgctcactct 1050

DRAFT - NOT FOR DISTRIBUTION

cagtgacaca gaggactcct tgcattttt gctgctttc cgagggctgc 1100
tggAACCCAG gagtgGGGGA ctaACCCAGG ttCCCTTgAg gCTCCAGATT 1150
ctacaccagg ggcagctact gcgagaactt caggccaatg tctcagccca 1200
ggaaccaggc tttgctgagg tgctgCCaa cctgacagtc caggagatgg 1250
actggctgggt gctgggggag ctgcagatgg ccctggagtg ggcaggcagg 1300
ccagggctgc gcatcagtgg acacattgtc gccaggaaga gctgcgacgt 1350
cctgcaaagt gtccttgtg gggctgatgc cctgatcccA gtccagacgg 1400
gtgctgccgg ctcagccagc ctcacgctgc taggaaatgg ctccctgatc 1450
tatcaggtgc aagtggtagg gacaagcagt gaggtggtgg ccatgacact 1500
ggagaccaag ctcagcgga gggatcagcg cactgtcctg tgccacatgg 1550
ctggactcca gccaggagga cacacggccg tgggtatctg ccctggctg 1600
ggtccccgag gggctcatat gctgctgcag aatgagctct tcctgaacgt 1650
gggcaccaag gacttcccag acggagagct tcggggcac gtggctgccc 1700
tgccctactg tggcatagc gcccGCCatg acacgctgcc cgtgccccta 1750
gcaggagccc tggctgtaacc ccctgtgaag agccaagcag cagggcacgc 1800
ctggcttcc ttggataccc actgtcacct gcactatgaa gtgctgctgg 1850
ctgggcttgg tggctcagaa caaggcactg tcactgcccA cctccttggg 1900
cctcctggaa cgccagggcc tcggcggctg ctgaagggat tctatggctc 1950
agaggcccag ggtgtggta aggacctgga gccggaactg ctgcggcacc 2000
tggcaaaagg catggcctcc ctgatgatca ccaccaaggg tagccccaga 2050
ggggagctcc gagggcaggt gcacatagcc aaccaatgtg aggttggcgg 2100
actgcgcctg gaggcggccg gggccgaggg ggtgcgggctg ctggggctc 2150
cggatacagc ctctgctgcg ccgcctgtgg tgcctggctc cccggcccta 2200
gcgcggccca aacctggtgg tccctggcgg ccccgagacc ccaacacatg 2250
cttcttcgag gggcagcagc gccccacgg ggctcgctgg ggcggccact 2300
acgacccgct ctgctcaactc tgcacactgcc agagacgaac ggtgatctgt 2350
gacccgggtgg tgtgcccacc gcccagctgc ccacacccgg tgcaggctcc 2400
cgaccagtgc tgccctgttt gccctgagaa acaagatgtc agagacttgc 2450
cagggctgcc aaggagccgg gacccaggag agggctgcta ttttgtatgg 2500

gaccggagct ggcgggcagc gggtaacgcgg tggcaccccg ttgtgcccc 2550
ctttggctta attaagtgtg ctgtctgcac ctgcaagggg ggcactggag 2600
aggtgcactg tgagaaggtg cagtgtcccc ggctggcctg tgcccagcct 2650
gtgcgtgtca accccaccga ctgctgaaa cagtgtccag tggggtcggg 2700
ggcccacccc cagctgggg accccatgca ggctgatggg ccccggggct 2750
gccgtttgc tggcagtgg ttcccagaga gtcagagctg gcacccctca 2800
gtgccccctt ttggagagat gagctgtatc acctgcagat gtggggcagg 2850
ggtgccctcac tgtgagcggg atgactgttc actgccactg tcctgtggct 2900
cgggaaagga gagtcgatgc tttcccgct gcacggccca ccggcggccc 2950
ccagagacca gaactgatcc agagctggag aaagaagccg aaggctctta 3000
gggagcagcc agagggccaa gtgaccaaga ggtatggggcc tgagctgggg 3050
aagggtggc atcgaggacc ttcttgatt ctccctgtggg aagcccagt 3100
ccttgctcc tctgtcctgc ctctactccc acccccacta cctctggaa 3150
ccacagctcc acaaggggaa gaggcagctg ggccagaccg aggtcacacg 3200
caactccaagt cctgcctgc caccctcgcc ctctgtcctg gaagccccac 3250
cccttcctc ctgtacataa tgtcaactggc ttgttggat ttttaattta 3300
tcttcactca gcaccaaggg ccccgacac tccactcctg ctgcccctga 3350
gctgagcaga gtcattattg gagagtttg tatttattaa aacatttctt 3400
tttcagtcaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 3441

<210> 7
<211> 954
<212> PRT
<213> Homo Sapien

<400> 7
Met Pro Ser Leu Pro Ala Pro Pro Ala Pro Leu Leu Leu Gly
1 5 10 15

Leu Leu Leu Leu Gly Ser Arg Pro Ala Arg Gly Ala Gly Pro Glu
20 25 30

Pro Pro Val Leu Pro Ile Arg Ser Glu Lys Glu Pro Leu Pro Val
35 40 45

Arg Gly Ala Ala Gly Cys Thr Phe Gly Gly Lys Val Tyr Ala Leu
50 55 60

Asp Glu Thr Trp His Pro Asp Leu Gly Gln Pro Phe Gly Val Met
65 70 75

Arg Cys Val Leu Cys Ala Cys Glu Ala Pro Gln Trp Gly Arg Arg
 80 85 90
 Thr Arg Gly Pro Gly Arg Val Ser Cys Lys Asn Ile Lys Pro Glu
 95 100 105
 Cys Pro Thr Pro Ala Cys Gly Gln Pro Arg Gln Leu Pro Gly His
 110 115 120
 Cys Cys Gln Thr Cys Pro Gln Glu Arg Ser Ser Ser Glu Arg Gln
 125 130 135
 Pro Ser Gly Leu Ser Phe Glu Tyr Pro Arg Asp Pro Glu His Arg
 140 145 150
 Ser Tyr Ser Asp Arg Gly Glu Pro Gly Ala Glu Glu Arg Ala Arg
 155 160 165
 Gly Asp Gly His Thr Asp Phe Val Ala Leu Leu Thr Gly Pro Arg
 170 175 180
 Ser Gln Ala Val Ala Arg Ala Arg Val Ser Leu Leu Arg Ser Ser
 185 190 195
 Leu Arg Phe Ser Ile Ser Tyr Arg Arg Leu Asp Arg Pro Thr Arg
 200 205 210
 Ile Arg Phe Ser Asp Ser Asn Gly Ser Val Leu Phe Glu His Pro
 215 220 225
 Ala Ala Pro Thr Gln Asp Gly Leu Val Cys Gly Val Trp Arg Ala
 230 235 240
 Val Pro Arg Leu Ser Leu Arg Leu Leu Arg Ala Glu Gln Leu His
 245 250 255
 Val Ala Leu Val Thr Leu Thr His Pro Ser Gly Glu Val Trp Gly
 260 265 270
 Pro Leu Ile Arg His Arg Ala Leu Ala Ala Glu Thr Phe Ser Ala
 275 280 285
 Ile Leu Thr Leu Glu Gly Pro Pro Gln Gln Gly Val Gly Gly Ile
 290 295 300
 Thr Leu Leu Thr Leu Ser Asp Thr Glu Asp Ser Leu His Phe Leu
 305 310 315
 Leu Leu Phe Arg Gly Leu Leu Glu Pro Arg Ser Gly Gly Leu Thr
 320 325 330
 Gln Val Pro Leu Arg Leu Gln Ile Leu His Gln Gly Gln Leu Leu
 335 340 345
 Arg Glu Leu Gln Ala Asn Val Ser Ala Gln Glu Pro Gly Phe Ala
 350 355 360
 Glu Val Leu Pro Asn Leu Thr Val Gln Glu Met Asp Trp Leu Val

TOTALS

365	370	375
Leu Gly Glu Leu Gln Met Ala Leu Glu Trp Ala Gly Arg Pro Gly		
380	385	390
Leu Arg Ile Ser Gly His Ile Ala Ala Arg Lys Ser Cys Asp Val		
395	400	405
Leu Gln Ser Val Leu Cys Gly Ala Asp Ala Leu Ile Pro Val Gln		
410	415	420
Thr Gly Ala Ala Gly Ser Ala Ser Leu Thr Leu Leu Gly Asn Gly		
425	430	435
Ser Leu Ile Tyr Gln Val Gln Val Val Gly Thr Ser Ser Glu Val		
440	445	450
Val Ala Met Thr Leu Glu Thr Lys Pro Gln Arg Arg Asp Gln Arg		
455	460	465
Thr Val Leu Cys His Met Ala Gly Leu Gln Pro Gly Gly His Thr		
470	475	480
Ala Val Gly Ile Cys Pro Gly Leu Gly Ala Arg Gly Ala His Met		
485	490	495
Leu Leu Gln Asn Glu Leu Phe Leu Asn Val Gly Thr Lys Asp Phe		
500	505	510
Pro Asp Gly Glu Leu Arg Gly His Val Ala Ala Leu Pro Tyr Cys		
515	520	525
Gly His Ser Ala Arg His Asp Thr Leu Pro Val Pro Leu Ala Gly		
530	535	540
Ala Leu Val Leu Pro Pro Val Lys Ser Gln Ala Ala Gly His Ala		
545	550	555
Trp Leu Ser Leu Asp Thr His Cys His Leu His Tyr Glu Val Leu		
560	565	570
Leu Ala Gly Leu Gly Gly Ser Glu Gln Gly Thr Val Thr Ala His		
575	580	585
Leu Leu Gly Pro Pro Gly Thr Pro Gly Pro Arg Arg Leu Leu Lys		
590	595	600
Gly Phe Tyr Gly Ser Glu Ala Gln Gly Val Val Lys Asp Leu Glu		
605	610	615
Pro Glu Leu Leu Arg His Leu Ala Lys Gly Met Ala Ser Leu Met		
620	625	630
Ile Thr Thr Lys Gly Ser Pro Arg Gly Glu Leu Arg Gly Gln Val		
635	640	645
His Ile Ala Asn Gln Cys Glu Val Gly Gly Leu Arg Leu Glu Ala		
650	655	660

DRAFT - NOT FOR RELEASE

Ala Gly Ala Glu Gly Val Arg Ala Leu Gly Ala Pro Asp Thr Ala
665 670 675

Ser Ala Ala Pro Pro Val Val Pro Gly Leu Pro Ala Leu Ala Pro
680 685 690

Ala Lys Pro Gly Gly Pro Gly Arg Pro Arg Asp Pro Asn Thr Cys
695 700 705

Phe Phe Glu Gly Gln Gln Arg Pro His Gly Ala Arg Trp Ala Pro
710 715 720

Asn Tyr Asp Pro Leu Cys Ser Leu Cys Thr Cys Gln Arg Arg Thr
725 730 735

Val Ile Cys Asp Pro Val Val Cys Pro Pro Pro Ser Cys Pro His
740 745 750

Pro Val Gln Ala Pro Asp Gln Cys Cys Pro Val Cys Pro Glu Lys
755 760 765

Gln Asp Val Arg Asp Leu Pro Gly Leu Pro Arg Ser Arg Asp Pro
770 775 780

Gly Glu Gly Cys Tyr Phe Asp Gly Asp Arg Ser Trp Arg Ala Ala
785 790 795

Gly Thr Arg Trp His Pro Val Val Pro Pro Phe Gly Leu Ile Lys
800 805 810

Cys Ala Val Cys Thr Cys Lys Gly Gly Thr Gly Glu Val His Cys
815 820 825

Glu Lys Val Gln Cys Pro Arg Leu Ala Cys Ala Gln Pro Val Arg
830 835 840

Val Asn Pro Thr Asp Cys Cys Lys Gln Cys Pro Val Gly Ser Gly
845 850 855

Ala His Pro Gln Leu Gly Asp Pro Met Gln Ala Asp Gly Pro Arg
860 865 870

Gly Cys Arg Phe Ala Gly Gln Trp Phe Pro Glu Ser Gln Ser Trp
875 880 885

His Pro Ser Val Pro Pro Phe Gly Glu Met Ser Cys Ile Thr Cys
890 895 900

Arg Cys Gly Ala Gly Val Pro His Cys Glu Arg Asp Asp Cys Ser
905 910 915

Leu Pro Leu Ser Cys Gly Ser Gly Lys Glu Ser Arg Cys Cys Ser
920 925 930

Arg Cys Thr Ala His Arg Arg Pro Pro Glu Thr Arg Thr Asp Pro
935 940 945

Glu Leu Glu Lys Glu Ala Glu Gly Ser

TOP SECRET//COMINT

950

<210> 8
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide probe

<400> 8
gactagttct agatcgcgag cggccgcctt tttttttt tttt 44

<210> 9
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 9
cggacgcgtg gggcctgcgc acccagct 28

<210> 10
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 10
gccgctcccc gaacgggcag cggctccttc tcagaa 36

<210> 11
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 11
ggcgcacagc acgcagcgca tcaccccgaa tggctc 36

<210> 12
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 12
tgctgccccca tccgttctga gaagga 26

<210> 13

NOTE: 80° = 15°C

<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 13
gcagggtgct caaacaggac ac 22

<210> 14
<211> 3231
<212> DNA
<213> Homo Sapien

<400> 14
ggcggagca g cctagccgc caccgtcgct ctgcagctc tcgtcgccac 50
tgccaccgccc gccgcgtca ctgcgtcctg gtcggcgtc ccgcgcctc 100
ccggccggcc atgcagcccc ggcgcgcca ggcgcgggt gcgcagctgc 150
tgcccgcgct ggccctgctg ctgcgtcgtc tcggagcggg gccccgaggc 200
agctccctgg ccaaccgggt gcccgcgcg ccctgtctg cgccgggcc 250
gtgcgcgcg cagccctgcc ggaatggggg tgtgtgcacc tcgcgcctg 300
agccggaccc gcagcacccg gccccgcgcg gcgcgcctgg ctacagctgc 350
acctgccccg cgggatctc cggcgccaa tgccagctt tgccagatcc 400
ttgtgccagc aacccttgct accatggcaa ctgcagcagc agcagcagca 450
gcagcagcga tggctacctc tgcatttgc atgaaggcta tgaaggccc 500
aactgtgaac aggacttcc cagtctccca gccactggct ggaccgaatc 550
catggcaccc cgacagcttc agcctgttcc tgctactcag gagcctgaca 600
aaatcctgcc tcgctctcag gcaacggta cactgcctac ctggcagccg 650
aaaacagggc agaaagttgt agaaatgaaa tggatcaag tggaggtgat 700
cccagatatt gcctgtggga atgccagttc taacagctct gcgggtggcc 750
gcctggatc ctttgaagtg ccacagaaca cctcagtcaa gattcggcaa 800
gatgccactg cctcactgat tttgcgttgg aaggcacgg ccacaggatt 850
ccaaacagtgc tccctcatag atggacgaag tgtgacccccc cttcaggctt 900
cagggggact ggtcctcctg gaggagatgc tcgccttggg gaataatcac 950
tttattgggt ttgtgaatga ttctgtgact aagtctattg tggctttgcg 1000
cttaactctg gtggtaagg tcagcacctg tgtgccgggg gagagtcacg 1050

TOP SECRET//COMINT

caaatgactt ggagtgttca ggaaaaggaa aatgcaccac gaagccgtca 1100
gaggcaactt tttcctgtac ctgtgaggag cagtacgtgg gtactttctg 1150
tgaagaatac gatgcttgcc agaggaaacc ttgccaaaac aacgcgagct 1200
gtattgatgc aaatgaaaag caagatggga gcaatttcac ctgtgtttgc 1250
cttcctgggtt atactggaga gctttgccag tccaagattg attactgcat 1300
cctagaccca tgcagaaaatg gagcaacatg catttccagt ctcagtggat 1350
tcacctgcca gtgtccagaa ggatacttcg gatctgcttg tgaagaaaag 1400
gtggacccct gcgcctcgtc tccgtgccag aacaacggca cctgctatgt 1450
ggacggggta cactttacct gcaactgcag cccgggcttc acagggccga 1500
cctgtgcccc gcttattgac ttctgtgccc tcagccccctg tgctcatggc 1550
acgtgcccga gcgtgggcac cagctacaaa tgcctctgtg atccaggtta 1600
ccatggcctc tactgtgagg aggaatataa tgagtgcctc tccgctccat 1650
gcctgaatgc agccacctgc agggacctcg ttaatggcta tgagtgtgtg 1700
tgcctggcag aatacaaagg aacacactgt gaattgtaca aggatccctg 1750
cgctaacgtc agctgtctga acggagccac ctgtgacagc gacggcctga 1800
atggcacgtg catctgtgca cccgggtta caggtgaaga gtgcgacatt 1850
gacataaatg aatgtgacag taacccctgc caccatggtg ggagctgcct 1900
ggaccagccc aatggttata actgccactg cccgcatggt tgggtggag 1950
caaactgtga gatccacctc caatggaagt ccggcacat ggcggagagc 2000
ctcaccaaca tgccacggca ctccctctac atcatcattt gagccctctg 2050
cgtggccttc atccttatgc tgatcatcct gatcgtgggg atttgcgcga 2100
tcagccgcatt tgaataccag gtttcttcca ggccagccta tgaggagttc 2150
tacaactgccc gcagcatcga cagcgagttc agcaatgcca ttgcattccat 2200
ccggcatgcc aggttggaa agaaatcccg gcctgcaatg tatgtatgtga 2250
gccccatcgc ctatgaagat tacagtcctg atgacaaaacc cttggtcaca 2300
ctgattaaaa ctaaagattt gtaatcttt tttggattat tttcaaaaa 2350
gatgagatac tacactcatt taaatattt taagaaaata aaaagcttaa 2400
gaaatttaaa atgctagctg ctcagagtt ttcaagtagaa tatttaagaa 2450
ctaattttct gcagcttta gtttggaaaa aatattttaa aaacaaaatt 2500

NOTE: This file is 100% DNA

tgtgaaacct atagacgatg ttttaatgtc ccttcagctc tctaaactgt 2550
gtgcttctac tagtgtgtgc tctttcact gtagacacta tcacgagacc 2600
cagattaatt tctgtggttg ttacagaata agtctaatac aggagaagtt 2650
tctgtttgac gtttgagtgc cggtttctg agtagagtt ggaaaaccac 2700
gtaacgtac atatgtatgtc taatagagta tacccgttac taaaaaagaa 2750
gtctgaaatg ttcgtttgtt ggaaaagaaaa ctatgtttt ttactattcc 2800
taacccgaat gaaatttagcc tttgccttat tctgtgcattt ggtaagtaac 2850
ttatctgc actgtttgtt tgaactttgtt ggaaacatttcc ttgcagttt 2900
gtttttgtca tttcgtaac agtcgtcgaa ctaggcctca aaaacatacg 2950
taacgaaaag gcctagcgag gcaaattctg attgatttga atctatattt 3000
ttctttaaaa agtcaagggt tctatattgtt gagtaaattt aatttacattt 3050
tgagttgtttt gttgctaaga ggttagtaaat gtaagagagt actggttcct 3100
tcagtagtga gtatctca tagtgcagct ttatcttcc ccaggatgtt 3150
tttggctg tatttggattt atatgtgcctt cttctgattt ttgctaattt 3200
ccaaccatat tgaataaaatg tgatcaagtc a 3231

<210> 15
<211> 737
<212> PRT
<213> Homo Sapien

<400> 15
Met Gln Pro Arg Arg Ala Gln Ala Pro Gly Ala Gln Leu Leu Pro
1 5 10 15
Ala Leu Ala Leu Leu Leu Leu Leu Gly Ala Gly Pro Arg Gly
20 25 30
Ser Ser Leu Ala Asn Pro Val Pro Ala Ala Pro Leu Ser Ala Pro
35 40 45
Gly Pro Cys Ala Ala Gln Pro Cys Arg Asn Gly Gly Val Cys Thr
50 55 60
Ser Arg Pro Glu Pro Asp Pro Gln His Pro Ala Pro Ala Gly Glu
65 70 75
Pro Gly Tyr Ser Cys Thr Cys Pro Ala Gly Ile Ser Gly Ala Asn
80 85 90
Cys Gln Leu Val Ala Asp Pro Cys Ala Ser Asn Pro Cys His His
95 100 105
Gly Asn Cys Ser Ser Ser Ser Ser Ser Asp Gly Tyr Leu

TOP SECRET - HHS-DOE

110	115	120
Cys Ile Cys Asn Glu Gly Tyr Glu Gly Pro Asn Cys Glu Gln Ala		
125	130	135
Leu Pro Ser Leu Pro Ala Thr Gly Trp Thr Glu Ser Met Ala Pro		
140	145	150
Arg Gln Leu Gln Pro Val Pro Ala Thr Gln Glu Pro Asp Lys Ile		
155	160	165
Leu Pro Arg Ser Gln Ala Thr Val Thr Leu Pro Thr Trp Gln Pro		
170	175	180
Lys Thr Gly Gln Lys Val Val Glu Met Lys Trp Asp Gln Val Glu		
185	190	195
Val Ile Pro Asp Ile Ala Cys Gly Asn Ala Ser Ser Asn Ser Ser		
200	205	210
Ala Gly Gly Arg Leu Val Ser Phe Glu Val Pro Gln Asn Thr Ser		
215	220	225
Val Lys Ile Arg Gln Asp Ala Thr Ala Ser Leu Ile Leu Leu Trp		
230	235	240
Lys Val Thr Ala Thr Gly Phe Gln Gln Cys Ser Leu Ile Asp Gly		
245	250	255
Arg Ser Val Thr Pro Leu Gln Ala Ser Gly Gly Leu Val Leu Leu		
260	265	270
Glu Glu Met Leu Ala Leu Gly Asn Asn His Phe Ile Gly Phe Val		
275	280	285
Asn Asp Ser Val Thr Lys Ser Ile Val Ala Leu Arg Leu Thr Leu		
290	295	300
Val Val Lys Val Ser Thr Cys Val Pro Gly Glu Ser His Ala Asn		
305	310	315
Asp Leu Glu Cys Ser Gly Lys Gly Lys Cys Thr Thr Lys Pro Ser		
320	325	330
Glu Ala Thr Phe Ser Cys Thr Cys Glu Glu Gln Tyr Val Gly Thr		
335	340	345
Phe Cys Glu Glu Tyr Asp Ala Cys Gln Arg Lys Pro Cys Gln Asn		
350	355	360
Asn Ala Ser Cys Ile Asp Ala Asn Glu Lys Gln Asp Gly Ser Asn		
365	370	375
Phe Thr Cys Val Cys Leu Pro Gly Tyr Thr Gly Glu Leu Cys Gln		
380	385	390
Ser Lys Ile Asp Tyr Cys Ile Leu Asp Pro Cys Arg Asn Gly Ala		
395	400	405

FOURTY EIGHT

Thr Cys Ile Ser Ser Leu Ser Gly Phe Thr Cys Gln Cys Pro Glu
410 415 420

Gly Tyr Phe Gly Ser Ala Cys Glu Glu Lys Val Asp Pro Cys Ala
425 430 435

Ser Ser Pro Cys Gln Asn Asn Gly Thr Cys Tyr Val Asp Gly Val
440 445 450

His Phe Thr Cys Asn Cys Ser Pro Gly Phe Thr Gly Pro Thr Cys
455 460 465

Ala Gln Leu Ile Asp Phe Cys Ala Leu Ser Pro Cys Ala His Gly
470 475 480

Thr Cys Arg Ser Val Gly Thr Ser Tyr Lys Cys Leu Cys Asp Pro
485 490 495

Gly Tyr His Gly Leu Tyr Cys Glu Glu Glu Tyr Asn Glu Cys Leu
500 505 510

Ser Ala Pro Cys Leu Asn Ala Ala Thr Cys Arg Asp Leu Val Asn
515 520 525

Gly Tyr Glu Cys Val Cys Leu Ala Glu Tyr Lys Gly Thr His Cys
530 535 540

Glu Leu Tyr Lys Asp Pro Cys Ala Asn Val Ser Cys Leu Asn Gly
545 550 555

Ala Thr Cys Asp Ser Asp Gly Leu Asn Gly Thr Cys Ile Cys Ala
560 565 570

Pro Gly Phe Thr Gly Glu Glu Cys Asp Ile Asp Ile Asn Glu Cys
575 580 585

Asp Ser Asn Pro Cys His His Gly Gly Ser Cys Leu Asp Gln Pro
590 595 600

Asn Gly Tyr Asn Cys His Cys Pro His Gly Trp Val Gly Ala Asn
605 610 615

Cys Glu Ile His Leu Gln Trp Lys Ser Gly His Met Ala Glu Ser
620 625 630

Leu Thr Asn Met Pro Arg His Ser Leu Tyr Ile Ile Ile Gly Ala
635 640 645

Leu Cys Val Ala Phe Ile Leu Met Leu Ile Ile Leu Ile Val Gly
650 655 660

Ile Cys Arg Ile Ser Arg Ile Glu Tyr Gln Gly Ser Ser Arg Pro
665 670 675

Ala Tyr Glu Glu Phe Tyr Asn Cys Arg Ser Ile Asp Ser Glu Phe
680 685 690

Ser Asn Ala Ile Ala Ser Ile Arg His Ala Arg Phe Gly Lys Lys

695

700

705

Ser Arg Pro Ala Met Tyr Asp Val Ser Pro Ile Ala Tyr Glu Asp
710 715 720

Tyr Ser Pro Asp Asp Lys Pro Leu Val Thr Leu Ile Lys Thr Lys
725 730 735

Asp Leu

<210> 16
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 16
tgtaaaacga cggccagttt aatagacctg caattattaa tct 43

<210> 17
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 17
caggaaacag ctagaccac ctgcacacct gcaaattcat t 41

<210> 18
<211> 508
<212> DNA
<213> Homo Sapien

<400> 18
ctctggaaagg tcacggccac aggattccaa cagtgtccc tcatacatgg 50
acgaaaagtgt gaccccccctt tcaggctttc agggggactg gtcctcctgg 100
aggagatgct cgccttgggg aataatcaact ttattgggtt tgtgaatgat 150
tctgtgacta agtctattgt ggcttgcgc ttaactctgg tggtaaggt 200
cagcacctgt gtgccggggg agagtcacgc aaatgacttg gagtgttcag 250
gaaaaggaaaa atgcaccacg aagccgtcag aggcaacttt ttcctgtacc 300
tgtgaggagc agtacgtggg tactttctgt gaagaatacg atgcttgcca 350
gaggaaacct tgccaaaaca acgcgagctg tattgatgca aatgaaaagc 400
aagatggagc caatttcacc tgtgtttgcc ttcctggta tactggagag 450
cttgccaaac cgaaactgaga ttggagcgaa cgacctacac cgaaactgaga 500

ప్రాణ వ్యాధి నుండి బాధక రోగాలు

tagggag 508

<210> 19
<211> 508
<212> DNA
<213> Homo Sapien

<400> 19
ctctggagg tcacggccac aggattccaa cagtgcgtccc tcatagatgg 50
acgaaaagtgt gaccccccctt tcaggctttc agggggactg gtcctcctgg 100
aggagatgct cgcccttgggg aataatcaact ttattggttt tgtgaatgat 150
tctgtgacta agtctattgt ggctttgcgc ttaactctgg tggtgaaggt 200
cagcacctgt gtgccggggg agagtcacgc aaatgacttg gagtgttcag 250
gaaaaggaaa atgcaccacg aagccgtcag aggcaacttt ttcctgtacc 300
tgtgaggagc agtacgtggg tactttctgt gaagaatacg atgcttgcca 350
gaggaaacct tgccaaaaca acgcgagctg tattgatgca aatgaaaagc 400
aagatggag caatttcacc tgtgtttgcc ttcctggta tactggagag 450
cttgc当地ac cgaactgaga ttggagcgaa cgacctacac cgaactgaga 500
tagggag 508

<210> 20
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 20
ctctggagg tcacggccac agg 23

<210> 21
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 21
ctcagttcgg ttggcaaagc tctc 24

<210> 22
<211> 69
<212> DNA
<213> Artificial Sequence

<220>

NOTE: 80° + 15°C = 95°C

<223> Synthetic oligonucleotide probe

<400> 22

cagtgcctcc tcatacatgg acgaaagtgt gaccccccctt tcaggcgaga 50
gccttgccaa ccgaactga 69

<210> 23

<211> 1520

<212> DNA

<213> Homo Sapien

<400> 23

gctgagtcgtc ctgcctctgc tgctgctgtc ccagcctgtta acctgtgcct 50
acaccacgccc agggccccccc agagccctca ccacgctggg cgccccccaga 100
gcccacaccca tgccgggcac ctacgctccc tcgaccacac tcagtagtcc 150
cagcacccag ggcctgcaag agcaggcactg ggcctgtatg cgggacttcc 200
cgctcgtgga cggccacaac gacctgcccc tggcctaag gcaggtttac 250
cagaaagggc tacaggatgt taacctgcgc aatttcagct acggccagac 300
cagcctggac aggcttagag atggcctcggt gggcgcccaag ttctggtcag 350
cctatgtgcc atgccagacc caggaccggg atgcctgcg cctcaccctg 400
gagcagattt acctcatacg ccgcattgtgt gcctcctatt ctgagctgga 450
gcttgtgacc tggctaaag ctctgaacga cactcagaaa ttggcctgcc 500
tcatcggtgt agaggggtggc cactcgctgg acaatagcct ctccatctta 550
cgtacccctt acatgctggg agtgcgtac ctgacgttca cccacaccc 600
caacacaccc tggcagaga gctccgctaa gggcgccac tccttctaca 650
acaacatcag cgggctgact gactttgggt agaagggtgt ggcagaaatg 700
aaccgcctgg gcatgatggt agacttatcc catgtctcag atgctgtggc 750
acggcgccctt ctggaagtgt cacaggcacc tgtgatcttc tcccactcgg 800
ctgccccgggg tgtgtcaac agtgcgtggc atgttcctga tgacatcctg 850
cagcttctga agaagaacgg tggcgctgtg atgggtgttt tgtccatggg 900
agtaatacag tgcaacccat cagccaatgt gtccactgtg gcagatcact 950
tcgaccacat caaggctgtc attggatcca agttcatcgg gattgggtgga 1000
gattatgatg gggccggcaa attccctcag gggctggaaag acgtgtccac 1050
atacccggtc ctgatagagg agttgctgag tcgtggctgg agtgaggaag 1100
agttcaggg tgtccctcggt ggaaacctgc tgcgggtctt cagacaagtg 1150

TOTALS 160

gaaaaggta c aggaagaaaa caaatggcaa agcccttgg aggacaagtt 1200
cccgatgag c agctgagca gttcctgcca ctccgacctc tcacgtctgc 1250
gtcagagaca gagtctgact tcaggccagg aactcactga gattccata 1300
cactggacag ccaagttacc agccaagtgg tcagtcttag agtcctcccc 1350
ccacatggcc ccagtccttg cagttgtggc cacctccca gtccttattc 1400
tgtggctctg atgacccagt tagtcctgcc agatgtcact gtagcaagcc 1450
acagacaccc cacaaggatc ccctgttgtg caggcacaaa tatttcctga 1500
aataaaatgtt ttggacatag 1520

<210> 24
<211> 433
<212> PRT
<213> Homo Sapien

<400> 24
Met Pro Gly Thr Tyr Ala Pro Ser Thr Thr Leu Ser Ser Pro Ser
1 5 10 15
Thr Gln Gly Leu Gln Glu Gln Ala Arg Ala Leu Met Arg Asp Phe
20 25 30
Pro Leu Val Asp Gly His Asn Asp Leu Pro Leu Val Leu Arg Gln
35 40 45
Val Tyr Gln Lys Gly Leu Gln Asp Val Asn Leu Arg Asn Phe Ser
50 55 60
Tyr Gly Gln Thr Ser Leu Asp Arg Leu Arg Asp Gly Leu Val Gly
65 70 75
Ala Gln Phe Trp Ser Ala Tyr Val Pro Cys Gln Thr Gln Asp Arg
80 85 90
Asp Ala Leu Arg Leu Thr Leu Glu Gln Ile Asp Leu Ile Arg Arg
95 100 105
Met Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala Lys
110 115 120
Ala Leu Asn Asp Thr Gln Lys Leu Ala Cys Leu Ile Gly Val Glu
125 130 135
Gly Gly His Ser Leu Asp Asn Ser Leu Ser Ile Leu Arg Thr Phe
140 145 150
Tyr Met Leu Gly Val Arg Tyr Leu Thr Leu Thr His Thr Cys Asn
155 160 165
Thr Pro Trp Ala Glu Ser Ser Ala Lys Gly Val His Ser Phe Tyr
170 175 180

SEQUENCE NUMBER

Asn Asn Ile Ser Gly Leu Thr Asp Phe Gly Glu Lys Val Val Ala
185 190 195
Glu Met Asn Arg Leu Gly Met Met Val Asp Leu Ser His Val Ser
200 205 210
Asp Ala Val Ala Arg Arg Ala Leu Glu Val Ser Gln Ala Pro Val
215 220 225
Ile Phe Ser His Ser Ala Ala Arg Gly Val Cys Asn Ser Ala Arg
230 235 240
Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Lys Asn Gly Gly
245 250 255
Val Val Met Val Ser Leu Ser Met Gly Val Ile Gln Cys Asn Pro
260 265 270
Ser Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Lys
275 280 285
Ala Val Ile Gly Ser Lys Phe Ile Gly Ile Gly Gly Asp Tyr Asp
290 295 300
Gly Ala Gly Lys Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr
305 310 315
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Gly Trp Ser Glu Glu
320 325 330
Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg
335 340 345
Gln Val Glu Lys Val Gln Glu Glu Asn Lys Trp Gln Ser Pro Leu
350 355 360
Glu Asp Lys Phe Pro Asp Glu Gln Leu Ser Ser Ser Cys His Ser
365 370 375
Asp Leu Ser Arg Leu Arg Gln Arg Gln Ser Leu Thr Ser Gly Gln
380 385 390
Glu Leu Thr Glu Ile Pro Ile His Trp Thr Ala Lys Leu Pro Ala
395 400 405
Lys Trp Ser Val Ser Glu Ser Ser Pro His Met Ala Pro Val Leu
410 415 420
Ala Val Val Ala Thr Phe Pro Val Leu Ile Leu Trp Leu
425 430

<210> 25
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

F0E5E8E0

```
<400> 25
agtctggtc agcctatgtg cc 22

<210> 26
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 26
cgatggtg tctttgtcca tggg 24

<210> 27
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 27
ctccaccaat cccgatgaac ttgg 24

<210> 28
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 28
gaggcattt acctcatacg ccgcattgtt gcctcctatt ctgagctgga 50

<210> 29
<211> 1416
<212> DNA
<213> Homo Sapien

<400> 29
aaaacctata aatattccgg attattcata ccgtccccacc atcgggcgcg 50
gatccgcggc cgcaattct aaaccaacat gccgggcacc tacgtccct 100
cgaccacact cagtagtccc agcacccagg gcctgcaaga gcaggcacgg 150
gccctgatgc gggacttccc gtcgtggac ggccacaacg acctgcccct 200
ggcctaagg caggttacc agaaagggtt acaggatgtt aacctgcgca 250
atttcagcta cggccagacc agcctggaca ggcttagaga tggcctcgtg 300
ggcgcccagt tctggtcagc ctatgtgcca tgccagaccc aggaccggga 350
tgccctgcgc ctcaccctgg agcagattga cctcatacgc cgcatgttg 400
```

TOP SECRET//COMINT

cctccttattc tgagctggag cttgtgacct cggtctaaagc tctgaacgc 450
actcagaaaat tggcctgcct catcggtgta gagggtggcc actcgctgga 500
caatagcctc tccatcttac gtaccttcta catgctggga gtgcgctacc 550
tgacgctcac ccacacctgc aacacaccct gggcagagag ctccgctaaag 600
ggcgtccact ctttctacaa caacatcagc gggctgactg actttggtga 650
gaaggtggtg gcagaaaatga accgcctggg catgatggta gacttatccc 700
atgtctcaga tgctgtggca cggcgggccc tggaagtgtc acaggcacct 750
gtgatcttct cccactcggc tgccccgggt gtgtcaaca gtgctcgaa 800
tgttcctgat gacatcctgc agttctgaa gaagaacggt ggcgtcgta 850
tgggtgtctt gtccatggga gtaatacagt gcaacccatc agccaatgtg 900
tccactgtgg cagatcactt cgaccacatc aaggctgtca ttggatccaa 950
gttcatcggg attgggtggag attatgatgg ggccggcaaa ttccctcagg 1000
ggcttggaaaga cgtgtccaca tacccggtcc tgatagagga gttgctgagt 1050
cgtggctgga gtgaggaaga gcttcagggt gtccttcgtg gaaacctgct 1100
gcgggtcttc agacaagtgg aaaaggtaca ggaagaaaaac aaatggcaaa 1150
gcccttggga ggacaagttc ccggatgagc agctgagcag ttccctgccac 1200
tccgacctct cacgtctgct tcagagacag agtctgactt caggccagga 1250
actcaactgag attcccatac actggacagc caagttacca gccaaagtgg 1300
cagtctcaga gtcctcccc caccctgaca aaactcacac atgcccacccg 1350
tgcccagcac ctgaactcct ggggggaccc tcagtcttcc tcttcccccc 1400
aaaacccaag gacacc 1416

<210> 30
<211> 446
<212> PRT
<213> Homo Sapien

<400> 30
Met Pro Gly Thr Tyr Ala Pro Ser Thr Thr Leu Ser Ser Pro Ser
1 5 10 15
Thr Gln Gly Leu Gln Glu Gln Ala Arg Ala Leu Met Arg Asp Phe
20 25 30
Pro Leu Val Asp Gly His Asn Asp Leu Pro Leu Val Leu Arg Gln
35 40 45
Val Tyr Gln Lys Gly Leu Gln Asp Val Asn Leu Arg Asn Phe Ser

TOTAL NUMBER OF AMINO ACIDS

50	55	60
Tyr Gly Gln Thr Ser Leu Asp Arg Leu Arg Asp Gly Leu Val Gly		
65	70	75
Ala Gln Phe Trp Ser Ala Tyr Val Pro Cys Gln Thr Gln Asp Arg		
80	85	90
Asp Ala Leu Arg Leu Thr Leu Glu Gln Ile Asp Leu Ile Arg Arg		
95	100	105
Met Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala Lys		
110	115	120
Ala Leu Asn Asp Thr Gln Lys Leu Ala Cys Leu Ile Gly Val Glu		
125	130	135
Gly Gly His Ser Leu Asp Asn Ser Leu Ser Ile Leu Arg Thr Phe		
140	145	150
Tyr Met Leu Gly Val Arg Tyr Leu Thr Leu Thr His Thr Cys Asn		
155	160	165
Thr Pro Trp Ala Glu Ser Ser Ala Lys Gly Val His Ser Phe Tyr		
170	175	180
Asn Asn Ile Ser Gly Leu Thr Asp Phe Gly Glu Lys Val Val Ala		
185	190	195
Glu Met Asn Arg Leu Gly Met Met Val Asp Leu Ser His Val Ser		
200	205	210
Asp Ala Val Ala Arg Arg Ala Leu Glu Val Ser Gln Ala Pro Val		
215	220	225
Ile Phe Ser His Ser Ala Ala Arg Gly Val Cys Asn Ser Ala Arg		
230	235	240
Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Lys Asn Gly Gly		
245	250	255
Val Val Met Val Ser Leu Ser Met Gly Val Ile Gln Cys Asn Pro		
260	265	270
Ser Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Lys		
275	280	285
Ala Val Ile Gly Ser Lys Phe Ile Gly Ile Gly Gly Asp Tyr Asp		
290	295	300
Gly Ala Gly Lys Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr		
305	310	315
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Gly Trp Ser Glu Glu		
320	325	330
Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg		
335	340	345

Gln Val Glu Lys Val Gln Glu Glu Asn Lys Trp Gln Ser Pro Leu
350 355 360
Glu Asp Lys Phe Pro Asp Glu Gln Leu Ser Ser Ser Cys His Ser
365 370 375
Asp Leu Ser Arg Leu Arg Gln Arg Gln Ser Leu Thr Ser Gly Gln
380 385 390
Glu Leu Thr Glu Ile Pro Ile His Trp Thr Ala Lys Leu Pro Ala
395 400 405
Lys Trp Ser Val Ser Glu Ser Ser Pro His Pro Asp Lys Thr His
410 415 420
Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
425 430 435
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
440 445

<210> 31
<211> 1790
<212> DNA
<213> Homo Sapien

<400> 31
cgccccagcga cgtgcgggcg gcctggcccg cgccctcccg cgcccgccct 50
gcgtcccgcg ccctgcgcca cccgcgcga gccgcagccc gccgcgcgc 100
cccgccagcg cccggcccat gccegcgcgc cgcgggggcc cccgcgccca 150
atccgcgcgg cggccgcgc cgttgctgcc cctgctgctg ctgctctgcg 200
tcctcggggc gccgcgagcc ggatcaggag cccacacagc tgtgatcagt 250
ccccaggatc ccacgcttct catcggtctcc tccctgctgg ccacctgctc 300
agtgcacgga gaccacccag gagccaccgc cgagggcctc tactggaccc 350
tcaacgggcg ccgcctgccc cctgagctct cccgtgtact caacgcctcc 400
accttggctc tggccctggc caacctaatt gggtccaggc agcggtcggg 450
ggacaacctc gtgtgccacg cccgtgacgg cagcatcctg gctggctct 500
gcctctatgt tggcctgccc ccagagaaac ccgtcaacat cagctgctgg 550
tccaagaaca tgaaggactt gacctgccgc tggacgcccag gggcccacgg 600
ggagacacctc ctccacacca actactccct caagtacaag ctttaggttgt 650
atggccagga caacacatgt gaggagtacc acacagtggg gccccactcc 700
tgccacatcc ccaaggaccc ggctctcttt acgcctatg agatctgggt 750
ggaggccacc aaccgcctgg gctctgccc ctcggatgtc ctcacgcgtgg 800

TOP SECRET - HUMAN GENOME

atatcctgga tgtggtgacc acggacccccc cgcccgacgt gcacgtgagc 850
cgcgtcgaaaa gcttggagga ccagctgagc gtgcgctggg tgtcgccacc 900
cgccctcaag gatttcctct ttcaagccaa ataccagatc cgctaccgag 950
tggaggacag tgtggactgg aaggtggtgg acgatgtgag caaccagacc 1000
tcctgcccgc tggccggcct gaaacccggc accgtgtact tcgtgcaagt 1050
gcgcgtgcaac ccctttggca tctatggctc caagaaagcc gggatctgga 1100
gtgagtgagg ccacccaca gccgcctcca ctccccgcag tgagcgcccg 1150
ggcccgccgcg gcggggcggt cgaaccgcgg ggccggagagc cgagctcggg 1200
gccgggtgcgg cgcgagctca agcagttcct gggctggctc aagaagcacg 1250
cgtactgctc caacctcagc ttccgcctct acgaccagtg gcgagcctgg 1300
atgcagaagt cgacacaagac ccgcaaccag gacgagggga tcctgccctc 1350
ggcagacgg ggcacggcga gaggtcctgc cagataagct gtaggggctc 1400
aggccacccct ccctgccacg tggagacgca gaggccgaac ccaaactggg 1450
gccacccctcg taccctcaact tcagggcacc tgagccaccc tcagcaggag 1500
ctggggtgtgc ccctgagctc caacggccat aacagctctg actcccacgt 1550
gaggccaccc ttgggtgcac cccagtggt gtgtgtgtgt gtgtgaggg 1600
tggtttagtt gcctagaacc cctgccaggg ctgggggtga gaaggggagt 1650
cattactccc cattacctag ggcccctcca aaagagtctt tttaaataaaa 1700
tgagctattt aggtgctgtg attgtaaaaaaa aaaaaaaaaaaa 1750
aaaaaaaaaaa aaaaaaaaaaaa aaaaacaaaa aaaaaaaaaaaa 1790

<210> 32
<211> 422
<212> PRT
<213> Homo Sapien

<400> 32
Met Pro Ala Gly Arg Arg Gly Pro Ala Ala Gln Ser Ala Arg Arg
1 5 10 15

Pro Pro Pro Leu Leu Pro Leu Leu Leu Leu Cys Val Leu Gly
20 25 30

Ala Pro Arg Ala Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro
35 40 45

Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Leu Ala Thr Cys
50 55 60

PROTEIN SEQUENCE

Ser Val His Gly Asp Pro Pro Gly Ala Thr Ala Glu Gly Leu Tyr
65 70 75

Trp Thr Leu Asn Gly Arg Arg Leu Pro Pro Glu Leu Ser Arg Val
80 85 90

Leu Asn Ala Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly
95 100 105

Ser Arg Gln Arg Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp
110 115 120

Gly Ser Ile Leu Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro
125 130 135

Glu Lys Pro Val Asn Ile Ser Cys Trp Ser Lys Asn Met Lys Asp
140 145 150

Leu Thr Cys Arg Trp Thr Pro Gly Ala His Gly Glu Thr Phe Leu
155 160 165

His Thr Asn Tyr Ser Leu Lys Tyr Lys Leu Arg Trp Tyr Gly Gln
170 175 180

Asp Asn Thr Cys Glu Glu Tyr His Thr Val Gly Pro His Ser Cys
185 190 195

His Ile Pro Lys Asp Leu Ala Leu Phe Thr Pro Tyr Glu Ile Trp
200 205 210

Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg Ser Asp Val Leu
215 220 225

Thr Leu Asp Ile Leu Asp Val Val Thr Thr Asp Pro Pro Pro Asp
230 235 240

Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu Ser Val
245 250 255

Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln Ala
260 265 270

Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys
275 280 285

Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly
290 295 300

Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro
305 310 315

Phe Gly Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp
320 325 330

Ser His Pro Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly
335 340 345

Pro Gly Gly Gly Ala Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser

350 355 360

Gly Pro Val Arg Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys
365 370 375

Lys His Ala Tyr Cys Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln
380 385 390

Trp Arg Ala Trp Met Gln Lys Ser His Lys Thr Arg Asn Gln Asp
395 400 405

Glu Gly Ile Leu Pro Ser Gly Arg Arg Gly Thr Ala Arg Gly Pro
410 415 420

Ala Arg

<210> 33
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 33
cccgccccgac gtgcacgtga gcc 23

<210> 34
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 34
tgagccagcc caggaactgc ttg 23

<210> 35
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 35
caagtgcgtc gcaaccctt tggcatctat ggctccaaga aagccggat 50

<210> 36
<211> 1771
<212> DNA
<213> Homo Sapien

<400> 36
cccacgcgtc cgctgggttt agatcgagca accctctaaa agcagtttag 50

TOP SECRET - SOURCE

agtggtaaaa aaaaaaaaaa acacaccaaa cgctcgcagc cacaagg 100
atgaaatttc ttctggacat ctcctgtttt ctcggatgc tgatcgatcg 150
ctcccttagag tccttcgtga agcttttat tcctaagagg agaaaatcg 200
tcaccggcga aatcgtgctg attacaggag ctggcatgg aattgggaga 250
ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300
tataaataag catggactgg aggaaacagc tgccaaatgc aaggactgg 350
gtgccaagggt tcataccttt gtggtagact gcagcaaccg agaagatatt 400
tacagctctg caaagaaggt gaaggcagaa attggagatg ttagtatttt 450
agtaaataat gctgggttag tctatacatac agatttggttt gctacacaag 500
atcctcagat tgaaaagact tttgaagttt atgtacttgc acatttctgg 550
actacaaagg catttcttcc tgcaatgacg aagaataacc atggccatat 600
tgtcaactgtg gcttcggcag ctggacatgt ctcggcccccc ttcttactgg 650
cttactgttc aagcaagttt gctgctgtt gatttcataa aactttgaca 700
gatgaactgg ctgccttaca aataactgga gtcaaaacaa catgtctgtg 750
tcctaatttc gtaaacactg gttcatcaa aaatccaagt acaagttgg 800
gaccactct ggaacctgag gaagtggtaa acaggctgat gcatgggatt 850
ctgactgagc agaagatgat ttttattcca tcttctatag ctttttaac 900
aacattggaa aggatccttc ctgagcgtt cctggcagtt ttaaaacgaa 950
aaatcagtgt taagtttgat gcagttattt gatataaaat gaaagcgcaa 1000
taagcaccta gtttctgaa aactgattt ccaggttttag gttgatgtca 1050
tctaatacgatg ccagaattttt aatgtttgaa cttctgtttt ttcttaattat 1100
ccccattttct tcaatatcat ttttggggct ttggcagtct tcatttacta 1150
ccacttgttc tttagccaaa agctgattac atatgatata aacagagaaa 1200
tacctttaga ggtgacttta agaaaaatga agaaaaagaa ccaaaatgac 1250
tttattaaaa taatttccaa gattattttt ggctcacctg aaggcttgc 1300
aaaatttgcgta ccataaccgt ttatataaca tatatttttta tttttgattt 1350
cacttaaattt ttgtataattt tgtgtttttt tttctgttct acataaaaatc 1400
agaaaacttca agctctctaa ataaaaatgaa ggactatatc tagtggtatt 1450
tcacaatgaa tatcatgaac tctcaatggg taggtttcat cctaccatt 1500

gccactctgt ttcctgagag atacctcaca ttccaatgcc aaacatttct 1550
gcacaggaa gctagaggtg gatacacgtg ttgcaagtat aaaagcatca 1600
ctgggattta aggagaattg agagaatgta cccacaaaatg gcagcaataa 1650
taaatggatc acactaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1700
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1750
aaaaaaaaaa aaaaaaaaaa a 1771

<210> 37
<211> 300
<212> PRT
<213> Homo Sapien

<400> 37

Met	Lys	Phe	Leu	Leu	Asp	Ile	Leu	Leu	Leu	Pro	Leu	Leu	Ile	
1													15	
Val	Cys	Ser	Leu	Glu	Ser	Phe	Val	Lys	Leu	Phe	Ile	Pro	Lys	Arg
							20			25				30
Arg	Lys	Ser	Val	Thr	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly
							35			40				45
His	Gly	Ile	Gly	Arg	Leu	Thr	Ala	Tyr	Glu	Phe	Ala	Lys	Leu	Lys
					50				55				60	
Ser	Lys	Leu	Val	Leu	Trp	Asp	Ile	Asn	Lys	His	Gly	Leu	Glu	Glu
					65				70				75	
Thr	Ala	Ala	Lys	Cys	Lys	Gly	Leu	Gly	Ala	Lys	Val	His	Thr	Phe
					80				85				90	
Val	Val	Asp	Cys	Ser	Asn	Arg	Glu	Asp	Ile	Tyr	Ser	Ser	Ala	Lys
					95				100				105	
Lys	Val	Lys	Ala	Glu	Ile	Gly	Asp	Val	Ser	Ile	Leu	Val	Asn	Asn
					110				115				120	
Ala	Gly	Val	Val	Tyr	Thr	Ser	Asp	Leu	Phe	Ala	Thr	Gln	Asp	Pro
					125				130				135	
Gln	Ile	Glu	Lys	Thr	Phe	Glu	Val	Asn	Val	Leu	Ala	His	Phe	Trp
					140				145				150	
Thr	Thr	Lys	Ala	Phe	Leu	Pro	Ala	Met	Thr	Lys	Asn	Asn	His	Gly
					155				160				165	
His	Ile	Val	Thr	Val	Ala	Ser	Ala	Ala	Gly	His	Val	Ser	Val	Pro
					170				175				180	
Phe	Leu	Leu	Ala	Tyr	Cys	Ser	Ser	Lys	Phe	Ala	Ala	Val	Gly	Phe
					185				190				195	
His	Lys	Thr	Leu	Thr	Asp	Glu	Leu	Ala	Ala	Leu	Gln	Ile	Thr	Gly

200 205 210

Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly Phe
215 220 225

Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu
230 235 240

Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys
245 250 255

Met Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu
260 265 270

Arg Ile Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile
275 280 285

Ser Val Lys Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln
290 295 300

<210> 38

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 38

ggtaaggca gaaattggag atg 23

<210> 39

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 39

atcccatgca tcagcctgtt tacc 24

<210> 40

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 40

gctggtag tctatacatc agattttttt gctacacaag atcctcag 48

<210> 41

<211> 1377

<212> DNA

<213> Homo Sapien

TOP SECRET

<400> 41
gactagttct cttggagtct gggaggagga aagcggagcc ggcagggagc 50
gaaccaggac tggggtgacg gcagggcagg gggcgctgg ccggggagaa 100
gcgcgggggc tggagcacca ccaactggag ggtccggagt agcgagcgcc 150
ccgaaggagg ccatacgaaaa gcccggaggg gggactgcga gaggaccccg 200
gcgtccgggc tccccgtgcc agcgctatga ggccactcct cgtcctgctg 250
ctccctgggcc tggcgccgg ctgcggggca ctggacgaca acaagatccc 300
cagcctctgc ccggggcacc ccggccttcc aggacacgccc ggccaccatg 350
gcagccaggg cttggccggc cgcgatggcc ggcacggccc cgacggcg 400
cccggggctc cgggagagaa aggcgagggc gggaggccgg gactgcccgg 450
acctcgaggg gaccccgccc cgcgaggaga ggcccggaccc gcccggccca 500
ccgggcctgc cggggagtgc tcggtgccctc cgcgatccgc cttcagcgcc 550
aagcgctccg agagccgggt gcctccgccc tctgacgcac cttgcctt 600
cgaccgcgtg ctggtaacg agcagggaca ttacgacgccc gtcaccggca 650
agttcacctg ccaggtgcct ggggtctact acttcgcccgt ccatgccacc 700
gtctaccggg ccagcctgca gtttgatctg gtgaagaatg gcgaatccat 750
tgccctttc ttccagttt tcgggggggtg gcccaagcca gcctcgctct 800
cgggggggggc catggtgagg ctggagccctg aggaccaagt gtgggtgcag 850
gtgggtgtgg gtgactacat tggcatctat gccagcatca agacagacag 900
caccttctcc ggatttctgg tgtactccga ctggcacagc tccccagtc 950
ttgcttagtg cccactgcaa agttagctca tgctctact cctagaagga 1000
gggtgtgagg ctgacaacca ggtcatccag gagggctggc cccccctggaa 1050
tattgtaat gactagggag gtggggtaga gcactctccg tcctgctgct 1100
ggcaaggaat gggAACAGTG GCTGTCTGCG ATCAGGTCTG GCAGCATGGG 1150
gcagtggctg gatttctgcc caagaccaga ggagtgtgt gtgctggcaa 1200
gtgttaagtcc cccagttgtctggc ctgggtccagg agcccacgggt ggggtgtct 1250
cttcctggtc ctctgcttct ctggatccctc cccacccct cctgctcctg 1300
ggggccggccc ttttctcaga gatcactcaa taaacctaag aaccctcata 1350
aaaaaaaaaaa aaaaaaaaaa aaaaaaaa 1377

<210> 42

TOP SECRET//COMINT

<211> 243
<212> PRT
<213> Homo Sapien

<400> 42

Met	Arg	Pro	Leu	Leu	Val	Leu	Leu	Leu	Gly	Leu	Ala	Ala	Gly	
1					5			10					15	
Ser	Pro	Pro	Leu	Asp	Asp	Asn	Lys	Ile	Pro	Ser	Leu	Cys	Pro	Gly
								20			25		30	
His	Pro	Gly	Leu	Pro	Gly	Thr	Pro	Gly	His	His	Gly	Ser	Gln	Gly
								35			40		45	
Leu	Pro	Gly	Arg	Asp	Gly	Arg	Asp	Gly	Arg	Asp	Gly	Ala	Pro	Gly
								50			55		60	
Ala	Pro	Gly	Glu	Lys	Gly	Glu	Gly	Gly	Arg	Pro	Gly	Leu	Pro	Gly
								65			70		75	
Pro	Arg	Gly	Asp	Pro	Gly	Pro	Arg	Gly	Glu	Ala	Gly	Pro	Ala	Gly
								80			85		90	
Pro	Thr	Gly	Pro	Ala	Gly	Glu	Cys	Ser	Val	Pro	Pro	Arg	Ser	Ala
								95			100		105	
Phe	Ser	Ala	Lys	Arg	Ser	Glu	Ser	Arg	Val	Pro	Pro	Pro	Ser	Asp
								110			115		120	
Ala	Pro	Leu	Pro	Phe	Asp	Arg	Val	Leu	Val	Asn	Glu	Gln	Gly	His
								125			130		135	
Tyr	Asp	Ala	Val	Thr	Gly	Lys	Phe	Thr	Cys	Gln	Val	Pro	Gly	Val
								140			145		150	
Tyr	Tyr	Phe	Ala	Val	His	Ala	Thr	Val	Tyr	Arg	Ala	Ser	Leu	Gln
								155			160		165	
Phe	Asp	Leu	Val	Lys	Asn	Gly	Glu	Ser	Ile	Ala	Ser	Phe	Phe	Gln
								170			175		180	
Phe	Phe	Gly	Gly	Trp	Pro	Lys	Pro	Ala	Ser	Leu	Ser	Gly	Gly	Ala
								185			190		195	
Met	Val	Arg	Leu	Glu	Pro	Glu	Asp	Gln	Val	Trp	Val	Gln	Val	Gly
								200			205		210	
Val	Gly	Asp	Tyr	Ile	Gly	Ile	Tyr	Ala	Ser	Ile	Lys	Thr	Asp	Ser
								215			220		225	
Thr	Phe	Ser	Gly	Phe	Leu	Val	Tyr	Ser	Asp	Trp	His	Ser	Ser	Pro
								230			235		240	
Val	Phe	Ala												

<210> 43
<211> 24

DRAFT Sequence Database

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 43
tacaggccca gtcaggacca gggg 24

<210> 44
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 44
agccagcctc gctctcg 18

<210> 45
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 45
gtctgcgatc aggtctgg 18

<210> 46
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 46
gaaagaggca atggattcgc 20

<210> 47
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 47
gacttacact tgccagcaca gcac 24

<210> 48
<211> 45
<212> DNA
<213> Artificial Sequence

TOP SECRET

<220>

<223> Synthetic oligonucleotide probe

<400> 48

ggagcaccac caactggagg gtccggagta gcgagcgccc cgaag 45

<210> 49

<211> 1876

<212> DNA

<213> Homo Sapien

<400> 49

ctctttgtc caccagccca gcctgactcc tggagattgt gaatagctcc 50

atccagcctg agaaacaagc cgggtggctg agccaggctg tgcacggagc 100

acctgacggg cccaacagac ccatgctgca tccagagacc tccccctggcc 150

gggggcatct cctggctgtg ctcctggccc tccttggcac cacctggca 200

gaggtgtggc caccggcagct gcaggagcag gctccgatgg ccggagccct 250

gaacaggaag gagagtttct tgctcctctc cctgcacaac cgccctgcgca 300

gctgggtcca gccccctgctg gctgacatgc ggaggctgga ctggagtgcac 350

agcctggccc aactggctca agccaggcga gccctctgtg gaatcccaac 400

cccgagcctg gcatccggcc tgtggcgcac cctgcaagtg ggctggaaaca 450

tgcagctgct gccccggggc ttggcgtctt ttgttgaagt ggtcagcccta 500

tggtttgcag aggggcagcg gtacagccac gcggcaggag agtgtgctcg 550

caacgccacc tgcacccact acacgcagct cgtgtggcc acctcaagcc 600

agctggctg tggccggcac ctgtgctctg caggccagac agcgatagaa 650

gcctttgtct gtgcctactc ccccgaggc aactgggagg tcaacggaa 700

gacaatcatc ccctataaga agggtgctg gtgtcgctc tgcacagcca 750

gtgtctcagg ctgcttcaaa gcctgggacc atgcaggggg gctctgtgag 800

gtccccagga atccttgcg catgagctgc cagaaccatg gacgtctcaa 850

catcagcacc tgccactgcc actgtcccc tggctacacg ggcagatact 900

gccaagtgag gtgcagcctg cagtgtgtgc acggccggtt ccgggaggag 950

gagtgctcggt gcgtctgtga catcggtac gggggagccc agtgtgccac 1000

caaggtgcattttcc acacctgtga cctgaggatc gacggagact 1050

gcttcatgggt gtcttcagag gcagacaccc attacagagc caggatgaaa 1100

tgtcagagga aaggcgggggt gctggcccag atcaagagcc agaaagtgcac 1150

DRAFT

ggacatcctc gccttctatc tggccgcct ggagaccacc aacgaggta 1200
ctgacagtga ctgcgagacc aggaacttct ggatcggtcacctacaag 1250
accgccaagg actccttcg ctggccaca ggggagcacc aggccttcac 1300
cagtttgcc tttggcagc ctgacaacca cgggctggtg tggctgagtg 1350
ctgccatggg gtttggcaac tgcgtggagc tgcaaggcttc agctgccttc 1400
aactggaacg accagcgctg caaaacccga aaccgttaca tctgccagtt 1450
tgcccaggag cacatctccc ggtggggccc agggctcgtga ggcctgacca 1500
catggctccc tcgcctgccc tggagcacc ggctctgctt acctgtctgc 1550
ccacctgtct ggaacaaggg ccaggttaag accacatgcc tcatgtccaa 1600
agaggtctca gaccttgcac aatgccagaa gttggcaga gagaggcagg 1650
gaggccagtg agggccaggg agtgagtgtt agaagaagct gggcccttc 1700
gcctgctttt gattggaaag atgggcttca attagatggc gaaggagagg 1750
acaccgcccag tggtccaaaa aggctgtctt cttcacctg gcccagaccc 1800
tgtgggcag cgagacttcc ctgtggcatg aaccccacgg ggtattaaat 1850
tatgaatca ctgaaaaaaaaaaaaa 1876

<210> 50

<211> 455

<212> PRT

<213> Homo Sapien

<400> 50

Met Leu His Pro Glu Thr Ser Pro Gly Arg Gly His Leu Leu Ala
1 5 10 15

Val Leu Leu Ala Leu Leu Gly Thr Thr Trp Ala Glu Val Trp Pro
20 25 30

Pro Gln Leu Gln Glu Gln Ala Pro Met Ala Gly Ala Leu Asn Arg
35 40 45

Lys Glu Ser Phe Leu Leu Ser Leu His Asn Arg Leu Arg Ser
50 55 60

Trp Val Gln Pro Pro Ala Ala Asp Met Arg Arg Leu Asp Trp Ser
65 70 75

Asp Ser Leu Ala Gln Leu Ala Gln Ala Arg Ala Ala Leu Cys Gly
80 85 90

Ile Pro Thr Pro Ser Leu Ala Ser Gly Leu Trp Arg Thr Leu Gln
95 100 105

Val Gly Trp Asn Met Gln Leu Leu Pro Ala Gly Leu Ala Ser Phe

TOP SECRET//NOFORN

110	115	120
Val Glu Val Val Ser Leu Trp Phe Ala	Glu Gly Gln Arg Tyr	Ser
125	130	135
His Ala Ala Gly Glu Cys Ala Arg Asn	Ala Thr Cys Thr His Tyr	
140	145	150
Thr Gln Leu Val Trp Ala Thr Ser Ser	Gln Leu Gly Cys Gly Arg	
155	160	165
His Leu Cys Ser Ala Gly Gln Thr Ala	Ile Glu Ala Phe Val Cys	
170	175	180
Ala Tyr Ser Pro Gly Gly Asn Trp Glu	Val Asn Gly Lys Thr Ile	
185	190	195
Ile Pro Tyr Lys Lys Gly Ala Trp Cys	Ser Leu Cys Thr Ala Ser	
200	205	210
Val Ser Gly Cys Phe Lys Ala Trp Asp	His Ala Gly Gly Leu Cys	
215	220	225
Glu Val Pro Arg Asn Pro Cys Arg Met	Ser Cys Gln Asn His Gly	
230	235	240
Arg Leu Asn Ile Ser Thr Cys His Cys	His Cys Pro Pro Gly Tyr	
245	250	255
Thr Gly Arg Tyr Cys Gln Val Arg Cys	Ser Leu Gln Cys Val His	
260	265	270
Gly Arg Phe Arg Glu Glu Cys Ser Cys	Val Cys Asp Ile Gly	
275	280	285
Tyr Gly Gly Ala Gln Cys Ala Thr Lys	Val His Phe Pro Phe His	
290	295	300
Thr Cys Asp Leu Arg Ile Asp Gly Asp	Cys Phe Met Val Ser Ser	
305	310	315
Glu Ala Asp Thr Tyr Tyr Arg Ala Arg	Met Lys Cys Gln Arg Lys	
320	325	330
Gly Gly Val Leu Ala Gln Ile Lys Ser	Gln Lys Val Gln Asp Ile	
335	340	345
Leu Ala Phe Tyr Leu Gly Arg Leu Glu	Thr Thr Asn Glu Val Thr	
350	355	360
Asp Ser Asp Phe Glu Thr Arg Asn Phe	Trp Ile Gly Leu Thr Tyr	
365	370	375
Lys Thr Ala Lys Asp Ser Phe Arg Trp	Ala Thr Gly Glu His Gln	
380	385	390
Ala Phe Thr Ser Phe Ala Phe Gly Gln	Pro Asp Asn His Gly Leu	
395	400	405

FOLEHOMO

Val Trp Leu Ser Ala Ala Met Gly Phe Gly Asn Cys Val Glu Leu
410 415 420
Gln Ala Ser Ala Ala Phe Asn Trp Asn Asp Gln Arg Cys Lys Thr
425 430 435
Arg Asn Arg Tyr Ile Cys Gln Phe Ala Gln Glu His Ile Ser Arg
440 445 450
Trp Gly Pro Gly Ser
455

<210> 51
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 51
agaacttct ggatcggct cacc 24

<210> 52
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 52
gggtctgggc caggttgaag agag 24

<210> 53
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 53
gccaaggact cttccgctg ggccacaggg gagcaccagg cttc 45

<210> 54
<211> 2331
<212> DNA
<213> Homo Sapien

<400> 54
cgacgcgtg ggctggcgca tgcaaagcgt gtcccgccgg gtccccgagc 50
gtcccgccgc ctgcggccgc catgctcctg ctgctggggc tgtgcctggg 100
gctgtccctg tgtgtgggt cgccaggaaga ggcgcagagc tggggccact 150
cttcggagca ggatggactc agggtcccga ggcaagttag actgttgtag 200

TOP SECRET

aggctgaaaa ccaaaccctt gatgacagaa ttctcagtga agtctaccat 250
catttccgt tatgccttca ctacggtttc ctgcagaatg ctgaacagag 300
cttctgaaga ccaggacatt gagttccaga tgcagattcc agctgcagct 350
ttcatcacca acttcaactat gcttattgga gacaagggtgt atcagggcga 400
aattacagag agagaaaaaga agagtggtga taggtaaaa gagaaaagga 450
ataaaaaccac agaagaaaat ggagagaagg ggactgaaat attcagagct 500
tctgcagtga ttcccagcaa ggacaaagcc gccttttcc tgagttatga 550
ggagcttctg cagaggcgcc tggcaagta cgagcacagc atcagcgtgc 600
ggccccagca gctgtccggg aggctgagcg tggacgtgaa tatectggag 650
agcgcgggca tcgcattccct ggaggtgctg ccgcattcaca acagcaggca 700
gaggggcagt gggcgcgggg aagatgattc tgggcctccc ccatctactg 750
tcattaacca aaatgaaaaca tttgccaaca taatttttaa acctactgta 800
gtacaacaag ccaggattgc ccagaatgga attttggag actttatcat 850
tagatatgac gtcaatagag aacagagcat tggggacatc caggttctaa 900
atggctattt tgtcaactac tttgctccta aagacatttc tcctttaccc 950
aagaatgtgg tattcgtgct tgacagcagt gcttctatgg tgggaaccaa 1000
actccggcag accaaggatg ccctttcac aatttccat gaccccgac 1050
cccaggaccg tttcagtatc attggattt ccaaccggat caaatatgg 1100
aaggaccact tgatatcagt cactccagac agcatcaggg atggaaagt 1150
gtacattcac catatgtcac ccactggagg cacagacatc aacggggccc 1200
tgcagagggc catcaggctc ctcacaact acgtggccca cagtggcatt 1250
ggagaccgga gcgtgtccct catcgcttcc ctgacggatg ggaagccac 1300
ggtcggggag acgcacaccc tcaagatcct caacaacacc cgagaggccg 1350
cccgaggcca agtctgcata ttcaccattt gcatcgccaa cgacgtggac 1400
ttcaggctgc tggagaaact gtcgctggag aactgtggcc tcacacggcg 1450
cgtgcacgag gaggaggacg caggctcgca gctcatcggt ttctacgatg 1500
aaatcaggac cccgctcctc tctgacatcc gcatcgatta tccccccagc 1550
tcagtggtgc aggccaccaa gaccctgttc cccaaactact tcaacggctc 1600
ggagatcatc attgcgggaa agctggtgga caggaagctg gatcacctgc 1650

BIOINFORMATICS

acgtggaggt caccgccagc aacagtaaga aattcatcat cctgaagaca 1700
gatgtgcctg tgcggcctca gaaggcaggg aaagatgtca caggaagccc 1750
caggccttgg a ggcqatggag agggggcacac caaccacatc gagcgtctct 1800
ggagctacct caccacaaag gagctgctga gtcctggct gcaaagtgac 1850
gatgaaccgg agaaggagcg gtcgcggcag cggcccccagg ccctggctgt 1900
gagctaccgc ttcctcaactc cttcacctc catgaagctg agggggccgg 1950
tccccacgcat ggtatggcctg gaggaggccc acggcatgtc ggctgccatg 2000
ggacccgaac cggtggtgca gagcgtgcga ggagctggca cgcagccagg 2050
acctttgctc aagaagccaa actccgtcaa aaaaaaacaa aacaaaacaa 2100
aaaaaaagaca tgggagagat ggtgttttc ctctccacca cctgggata 2150
cgatgagaag atggccacct gcaagccagg aagacggccc tcaccagaca 2200
ccatgtctgc tggcaccttg atcttgacc tcccaagcctc cagaactgtg 2250
agaaataaat gtgtttgtt taagctaaaa aaaaaaaaaa aaaaaaaaaa 2300
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 2331

<210> 55
<211> 694
<212> PRT
<213> Homo Sapien

<400> 55
Met Leu Leu Leu Leu Gly Leu Cys Leu Gly Leu Ser Leu Cys Val
1 5 10 15
Gly Ser Gln Glu Glu Ala Gln Ser Trp Gly His Ser Ser Glu Gln
20 25 30
Asp Gly Leu Arg Val Pro Arg Gln Val Arg Leu Leu Gln Arg Leu
35 40 45
Lys Thr Lys Pro Leu Met Thr Glu Phe Ser Val Lys Ser Thr Ile
50 55 60
Ile Ser Arg Tyr Ala Phe Thr Thr Val Ser Cys Arg Met Leu Asn
65 70 75
Arg Ala Ser Glu Asp Gln Asp Ile Glu Phe Gln Met Gln Ile Pro
80 85 90
Ala Ala Ala Phe Ile Thr Asn Phe Thr Met Leu Ile Gly Asp Lys
95 100 105
Val Tyr Gln Gly Glu Ile Thr Glu Arg Glu Lys Lys Ser Gly Asp
110 115 120

WORLDSLICER

Arg Val Lys Glu Lys Arg Asn Lys Thr Thr Glu Glu Asn Gly Glu
125 130 135
Lys Gly Thr Glu Ile Phe Arg Ala Ser Ala Val Ile Pro Ser Lys
140 145 150
Asp Lys Ala Ala Phe Phe Leu Ser Tyr Glu Glu Leu Leu Gln Arg
155 160 165
Arg Leu Gly Lys Tyr Glu His Ser Ile Ser Val Arg Pro Gln Gln
170 175 180
Leu Ser Gly Arg Leu Ser Val Asp Val Asn Ile Leu Glu Ser Ala
185 190 195
Gly Ile Ala Ser Leu Glu Val Leu Pro Leu His Asn Ser Arg Gln
200 205 210
Arg Gly Ser Gly Arg Gly Glu Asp Asp Ser Gly Pro Pro Pro Ser
215 220 225
Thr Val Ile Asn Gln Asn Glu Thr Phe Ala Asn Ile Ile Phe Lys
230 235 240
Pro Thr Val Val Gln Gln Ala Arg Ile Ala Gln Asn Gly Ile Leu
245 250 255
Gly Asp Phe Ile Ile Arg Tyr Asp Val Asn Arg Glu Gln Ser Ile
260 265 270
Gly Asp Ile Gln Val Leu Asn Gly Tyr Phe Val His Tyr Phe Ala
275 280 285
Pro Lys Asp Leu Pro Pro Leu Pro Lys Asn Val Val Phe Val Leu
290 295 300
Asp Ser Ser Ala Ser Met Val Gly Thr Lys Leu Arg Gln Thr Lys
305 310 315
Asp Ala Leu Phe Thr Ile Leu His Asp Leu Arg Pro Gln Asp Arg
320 325 330
Phe Ser Ile Ile Gly Phe Ser Asn Arg Ile Lys Val Trp Lys Asp
335 340 345
His Leu Ile Ser Val Thr Pro Asp Ser Ile Arg Asp Gly Lys Val
350 355 360
Tyr Ile His His Met Ser Pro Thr Gly Gly Thr Asp Ile Asn Gly
365 370 375
Ala Leu Gln Arg Ala Ile Arg Leu Leu Asn Lys Tyr Val Ala His
380 385 390
Ser Gly Ile Gly Asp Arg Ser Val Ser Leu Ile Val Phe Leu Thr
395 400 405
Asp Gly Lys Pro Thr Val Gly Glu Thr His Thr Leu Lys Ile Leu

TOP SECRET

410

415

420

Asn Asn Thr Arg Glu Ala Ala Arg Gly Gln Val Cys Ile Phe Thr
425 430 435

Ile Gly Ile Gly Asn Asp Val Asp Phe Arg Leu Leu Glu Lys Leu
440 445 450

Ser Leu Glu Asn Cys Gly Leu Thr Arg Arg Val His Glu Glu Glu
455 460 465

Asp Ala Gly Ser Gln Leu Ile Gly Phe Tyr Asp Glu Ile Arg Thr
470 475 480

Pro Leu Leu Ser Asp Ile Arg Ile Asp Tyr Pro Pro Ser Ser Val
485 490 495

Val Gln Ala Thr Lys Thr Leu Phe Pro Asn Tyr Phe Asn Gly Ser
500 505 510

Glu Ile Ile Ile Ala Gly Lys Leu Val Asp Arg Lys Leu Asp His
515 520 525

Leu His Val Glu Val Thr Ala Ser Asn Ser Lys Lys Phe Ile Ile
530 535 540

Leu Lys Thr Asp Val Pro Val Arg Pro Gln Lys Ala Gly Lys Asp
545 550 555

Val Thr Gly Ser Pro Arg Pro Gly Gly Asp Gly Glu Gly Asp Thr
560 565 570

Asn His Ile Glu Arg Leu Trp Ser Tyr Leu Thr Thr Lys Glu Leu
575 580 585

Leu Ser Ser Trp Leu Gln Ser Asp Asp Glu Pro Glu Lys Glu Arg
590 595 600

Leu Arg Gln Arg Ala Gln Ala Leu Ala Val Ser Tyr Arg Phe Leu
605 610 615

Thr Pro Phe Thr Ser Met Lys Leu Arg Gly Pro Val Pro Arg Met
620 625 630

Asp Gly Leu Glu Glu Ala His Gly Met Ser Ala Ala Met Gly Pro
635 640 645

Glu Pro Val Val Gln Ser Val Arg Gly Ala Gly Thr Gln Pro Gly
650 655 660

Pro Leu Leu Lys Lys Pro Asn Ser Val Lys Lys Lys Gln Asn Lys
665 670 675

Thr Lys Lys Arg His Gly Arg Asp Gly Val Phe Pro Leu His His
680 685 690

Leu Gly Ile Arg

□ □ □ □ □ □ □ □ □

```
<210> 56
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 56
gtgggaacca aactccggca gacc 24

<210> 57
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 57
cacatcgagg gtctctgg 18

<210> 58
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 58
agccgctcct tctccggttc atcg 24

<210> 59
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 59
tggaaaggacc acttgatatac agtcactcca gacagcatca gggatggg 48

<210> 60
<211> 1413
<212> DNA
<213> Homo Sapien

<400> 60
cggacgcgtg gggtgcccga catggcgagt gtagtgctgc cgagcggatc 50
ccagtgtgcg gcggcagcgg cggcggcggc gcctccggg ctccggcttc 100
tgctgttgct cttctccgcc gcggcactga tccccacagg tgatggcag 150
aatctgttta cgaaagacgt gacagtgtac gagggagagg ttgcgaccat 200
```

TOP SECRET

cagttgccaa gtcaataaga gtgacgactc tgtgattcag ctactgaatc 250
ccaacaggca gaccatttat ttcagggact tcaggcctt gaaggacagc 300
aggtttcagt tgctgaattt ttcttagcagt gaactcaaag tatcattgac 350
aacacgtctca atttctgatg aaggaagata ctttgccag ctctataccg 400
atcccccaca ggaaagttac accaccatca cagtcctggt cccaccacgt 450
aatctgatga tcgatatatcca gaaagacact gcggtgaaag gtgaggagat 500
tgaagtcaac tgcactgcta tggccagcaa gccagccacg actatcaggt 550
ggttcaaagg gaacacagag ctaaaaggca aatcgaggt ggaagagtgg 600
tcagacatgt acactgtgac cagtcagctg atgctgaagg tgcacaagga 650
ggacgatggg gtcccagtga tctgccaggt ggagcacccct gcggtcactg 700
gaaacctgca gaccacggg tatctagaag tacagtataa gcctcaagt 750
cacattcaga tgacttatcc tctacaaggc ttaacccggg aaggggacgc 800
gcttgagttt acatgtgaag ccatacgaa gccccagcct gtgatggtaa 850
cttgggtgag agtcgatgtat gaaatgcctc aacacgcccgt actgtctggg 900
cccaacctgt tcatcaataa cctaaacaaa acagataatg gtacataccg 950
ctgtgaagct tcaaacatag tggggaaagc tcactcggat tatatgctgt 1000
atgtatacga tccccccaca actatccctc ctcccacaac aaccaccacc 1050
accaccacca ccaccaccac caccatcctt accatcatca cagattcccg 1100
agcaggtgaa gaaggctcga tcagggcagt ggatcatgcc gtgatcggtg 1150
gcgtcggtgc ggtgggtgt ttcgcctatgc tgtgtttgt catcattctg 1200
gggcgttatt ttgccagaca taaaggtaca tactcactc atgaagccaa 1250
aggagccgat gacgcagcag acgcagacac agctataatc aatgcagaag 1300
gaggacagaa caactccgaa gaaaagaaaag agtacttcat cttagatcagc 1350
ctttttgttt caatgaggtg tccaaactggc cctatttaga tgataaaagag 1400
acagtgatata tgg 1413

<210> 61
<211> 440
<212> PRT
<213> Homo Sapien

<400> 61
Met Ala Ser Val Val Leu Pro Ser Gly Ser Gln Cys Ala Ala Ala
1 5 10 15

TOP SECRET - FINGERPRINTS

Ala Ala Ala Ala Ala Pro Pro Gly Leu Arg Leu Leu Leu Leu
20 25 30

Phe Ser Ala Ala Ala Leu Ile Pro Thr Gly Asp Gly Gln Asn Leu
35 40 45

Phe Thr Lys Asp Val Thr Val Ile Glu Gly Glu Val Ala Thr Ile
50 55 60

Ser Cys Gln Val Asn Lys Ser Asp Asp Ser Val Ile Gln Leu Leu
65 70 75

Asn Pro Asn Arg Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu
80 85 90

Lys Asp Ser Arg Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu
95 100 105

Lys Val Ser Leu Thr Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr
110 115 120

Phe Cys Gln Leu Tyr Thr Asp Pro Pro Gln Glu Ser Tyr Thr Thr
125 130 135

Ile Thr Val Leu Val Pro Pro Arg Asn Leu Met Ile Asp Ile Gln
140 145 150

Lys Asp Thr Ala Val Glu Gly Glu Glu Ile Glu Val Asn Cys Thr
155 160 165

Ala Met Ala Ser Lys Pro Ala Thr Thr Ile Arg Trp Phe Lys Gly
170 175 180

Asn Thr Glu Leu Lys Gly Lys Ser Glu Val Glu Glu Trp Ser Asp
185 190 195

Met Tyr Thr Val Thr Ser Gln Leu Met Leu Lys Val His Lys Glu
200 205 210

Asp Asp Gly Val Pro Val Ile Cys Gln Val Glu His Pro Ala Val
215 220 225

Thr Gly Asn Leu Gln Thr Gln Arg Tyr Leu Glu Val Gln Tyr Lys
230 235 240

Pro Gln Val His Ile Gln Met Thr Tyr Pro Leu Gln Gly Leu Thr
245 250 255

Arg Glu Gly Asp Ala Leu Glu Leu Thr Cys Glu Ala Ile Gly Lys
260 265 270

Pro Gln Pro Val Met Val Thr Trp Val Arg Val Asp Asp Glu Met
275 280 285

Pro Gln His Ala Val Leu Ser Gly Pro Asn Leu Phe Ile Asn Asn
290 295 300

Leu Asn Lys Thr Asp Asn Gly Thr Tyr Arg Cys Glu Ala Ser Asn

TOTAL LENGTH 50

305

310

315

Ile Val Gly Lys Ala His Ser Asp Tyr Met Leu Tyr Val Tyr Asp
320 325 330

Pro Pro Thr Thr Ile Pro Pro Pro Thr Thr Thr Thr Thr Thr Thr
335 340 345

Thr Thr Thr Thr Thr Ile Leu Thr Ile Ile Thr Asp Ser Arg
350 355 360

Ala Gly Glu Glu Gly Ser Ile Arg Ala Val Asp His Ala Val Ile
365 370 375

Gly Gly Val Val Ala Val Val Val Phe Ala Met Leu Cys Leu Leu
380 385 390

Ile Ile Leu Gly Arg Tyr Phe Ala Arg His Lys Gly Thr Tyr Phe
395 400 405

Thr His Glu Ala Lys Gly Ala Asp Asp Ala Ala Asp Ala Asp Thr
410 415 420

Ala Ile Ile Asn Ala Glu Gly Gly Gln Asn Asn Ser Glu Glu Lys
425 430 435

Lys Glu Tyr Phe Ile
440

<210> 62

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 62

ggcttctgct gttgctcttc tccg 24

<210> 63

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 63

gtacactgtg accagtcagc 20

<210> 64

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

TOMESOFT

```
<400> 64
atcatcacag attcccgagc 20

<210> 65
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 65
ttcaatctcc tcaccccca ccgc 24

<210> 66
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 66
atacgctgt ctgcgtctgc tgcg 24

<210> 67
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 67
cgccggactg atccccacag gtgatggca gaatctgtt acgaaagacg 50

<210> 68
<211> 2555
<212> DNA
<213> Homo Sapien

<400> 68
ggggcggttg gacgcggact cgaacgcagt tgcttcggga cccaggaccc 50
cctcgccccc gacccgccag gaaagactga ggccgcggcc tgccccgccc 100
ggctccctgc gccgcgcggc cctcccgaaa cagaagatgt gctccagggt 150
ccctctgctg ctggcgctgc tcctgtact ggcctgggg cctggggtgc 200
agggctgccc atccggctgc cagtgcagcc agccacagac agtcttctgc 250
actgcccccc aggggaccac ggtgccccga gacgtgccac ccgacacgg 300
ggggctgtac gtcttgaga acggcatcac catgctcgac gcaaggagct 350
ttggccggcct gccgggcctg cagtcctgg acctgtcaca gaaccagatc 400
```

TOEFL TEST

gccagcctgc gcctgccccg cctgctgctg ctggacctca gccacaacag 450
cctcctggcc ctggagccccg gcacccctgga cactgccaac gtggaggcgc 500
tgcggctggc tggctctgggg ctgcagcagc tggacgaggg gctcttcagc 550
cgcttgcgca acctccacga cctggatgtg tccgacaacc agctggagcg 600
agtgccacccgtatccgag gcctccgggg cctgacgcgc ctgcggctgg 650
ccggcaacac ccgcattgcc cagctgcggc ccgaggaccc ggccggcctg 700
gctgcccctgc aggagctgga tgtgagcaac ctaaggctgc aggccctgcc 750
tggcgaccc tcgggcctct tccccccgcct gcggctgctg gcagctgccc 800
gcaacccctt caactgcgtg tgccccctga gctgggttgg cccctgggtg 850
cgcgagagcc acgtcacact ggccagccct gaggagacgc gctgccactt 900
cccgcccaag aacgctggcc ggctgctct ggagcttgac tacgcccact 950
ttggctgccc agccaccacc accacagcca cagtgcac cacgaggccc 1000
gtggtgccgg agccccacagc cttgttttct agcttggctc ctacctggct 1050
tagccccaca gcgcggcca ctgaggcccc cagcccgccc tccactgccc 1100
caccgactgt agggcctgtc ccccaagcccc aggactgccc accgtccacc 1150
tgcctcaatg ggggcacatg ccacctgggg acacggcacc acctggcgtg 1200
cttgtgcccc gaaggcttca cgggcctgtc ctgtgagagc cagatgggc 1250
aggggacacg gcccagccct acaccagtca cgccgaggcc accacggtcc 1300
ctgaccctgg gcacccgagcc ggtgagcccc acctccctgc gcgtgggct 1350
gcagcgctac ctccaggggga gctccgtcga gtcaggagc ctccgtctca 1400
cctatcgcaa cctatcgggc cctgataagc ggctggtgac gctgcgactg 1450
cctgcctcgc tcgctgagta cacggtcacc cagctgcggc ccaacgcccac 1500
ttactccgtc tgtgtcatgc ctttggggcc cgggcgggtg ccggaggcgc 1550
aggaggcctg cggggaggcc catacaccctt cagccgtcca ctccaaccac 1600
gccccagtcg cccagggcccg cgagggcaac ctgcgcgtcc tcattgcgcc 1650
cgccctggcc gcgggtgtcc tggccgcgtc ggctgcgggtg ggggcagccct 1700
actgtgtgcg gcggggggcgg gccatggcag cagccgtca ggacaaagg 1750
caggtggggc caggggctgg gcccctggaa ctggagggag tgaaggccc 1800
cttggagcca ggcccgaaagg caacagaggg cggtggagag gcccctgccc 1850

TOP SECRET//COMINT

gcgggtctga gtgtgaggtg ccactcatgg gcttcccagg gcctggcctc 1900
cagtcacccc tccacgcaaa gccctacatc taagccagag agagacaggg 1950
cagctggggc cgggctctca gccagtgaga tggccagccc ctcctgctg 2000
ccacaccacg taagttctca gtcccaacct cggggatgtg tgcagacagg 2050
gctgtgtgac cacagctggg ccctgttccc tctggacctc ggtctcctca 2100
tctgtgagat gctgtggccc agctgacgag ccctaacgtc cccagaaccg 2150
agtgcctatg aggacagtgt cgcgcctgcc ctccgcaacg tgcagtccct 2200
gggcacggcg ggccctgcca tgtgctggta acgcatgcct gggccctgct 2250
gggctctccc actccaggcg gaccctgggg gccagtgaag gaagctcccg 2300
gaaagagcag agggagagcg gtaggcggc tgtgtgactc tagtcttggc 2350
cccaggaagc gaaggaacaa aagaaactgg aaaggaagat gctttaggaa 2400
catgtttgc tttttaaaaa tatatatata tttataagag atccttccc 2450
atttattctg ggaagatgtt tttcaaactc agagacaagg actttggttt 2500
ttgtaagaca aacgatgata tgaaggcctt ttgtaagaaa aaataaaaaaa 2550
aaaaaa 2555

<210> 69
<211> 598
<212> PRT
<213> Homo Sapien

<400> 69
Met Cys Ser Arg Val Pro Leu Leu Leu Pro Leu Leu Leu Leu
1 5 10 15
Ala Leu Gly Pro Gly Val Gln Gly Cys Pro Ser Gly Cys Gln Cys
20 25 30
Ser Gln Pro Gln Thr Val Phe Cys Thr Ala Arg Gln Gly Thr Thr
35 40 45
Val Pro Arg Asp Val Pro Pro Asp Thr Val Gly Leu Tyr Val Phe
50 55 60
Glu Asn Gly Ile Thr Met Leu Asp Ala Ser Ser Phe Ala Gly Leu
65 70 75
Pro Gly Leu Gln Leu Leu Asp Leu Ser Gln Asn Gln Ile Ala Ser
80 85 90
Leu Arg Leu Pro Arg Leu Leu Leu Asp Leu Ser His Asn Ser
95 100 105
Leu Leu Ala Leu Glu Pro Gly Ile Leu Asp Thr Ala Asn Val Glu

TOP SECRET//COMINT

110	115	120
Ala Leu Arg Leu Ala Gly Leu Gly Leu Gln Gln Leu Asp Glu Gly		
125	130	135
Leu Phe Ser Arg Leu Arg Asn Leu His Asp Leu Asp Val Ser Asp		
140	145	150
Asn Gln Leu Glu Arg Val Pro Pro Val Ile Arg Gly Leu Arg Gly		
155	160	165
Leu Thr Arg Leu Arg Leu Ala Gly Asn Thr Arg Ile Ala Gln Leu		
170	175	180
Arg Pro Glu Asp Leu Ala Gly Leu Ala Ala Leu Gln Glu Leu Asp		
185	190	195
Val Ser Asn Leu Ser Leu Gln Ala Leu Pro Gly Asp Leu Ser Gly		
200	205	210
Leu Phe Pro Arg Leu Arg Leu Leu Ala Ala Ala Arg Asn Pro Phe		
215	220	225
Asn Cys Val Cys Pro Leu Ser Trp Phe Gly Pro Trp Val Arg Glu		
230	235	240
Ser His Val Thr Leu Ala Ser Pro Glu Glu Thr Arg Cys His Phe		
245	250	255
Pro Pro Lys Asn Ala Gly Arg Leu Leu Leu Glu Leu Asp Tyr Ala		
260	265	270
Asp Phe Gly Cys Pro Ala Thr Thr Thr Ala Thr Val Pro Thr		
275	280	285
Thr Arg Pro Val Val Arg Glu Pro Thr Ala Leu Ser Ser Ser Leu		
290	295	300
Ala Pro Thr Trp Leu Ser Pro Thr Ala Pro Ala Thr Glu Ala Pro		
305	310	315
Ser Pro Pro Ser Thr Ala Pro Pro Thr Val Gly Pro Val Pro Gln		
320	325	330
Pro Gln Asp Cys Pro Pro Ser Thr Cys Leu Asn Gly Gly Thr Cys		
335	340	345
His Leu Gly Thr Arg His His Leu Ala Cys Leu Cys Pro Glu Gly		
350	355	360
Phe Thr Gly Leu Tyr Cys Glu Ser Gln Met Gly Gln Gly Thr Arg		
365	370	375
Pro Ser Pro Thr Pro Val Thr Pro Arg Pro Pro Arg Ser Leu Thr		
380	385	390
Leu Gly Ile Glu Pro Val Ser Pro Thr Ser Leu Arg Val Gly Leu		
395	400	405

Gln Arg Tyr Leu Gln Gly Ser Ser Val Gln Leu Arg Ser Leu Arg
410 415 420

Leu Thr Tyr Arg Asn Leu Ser Gly Pro Asp Lys Arg Leu Val Thr
425 430 435

Leu Arg Leu Pro Ala Ser Leu Ala Glu Tyr Thr Val Thr Gln Leu
440 445 450

Arg Pro Asn Ala Thr Tyr Ser Val Cys Val Met Pro Leu Gly Pro
455 460 465

Gly Arg Val Pro Glu Gly Glu Ala Cys Gly Glu Ala His Thr
470 475 480

Pro Pro Ala Val His Ser Asn His Ala Pro Val Thr Gln Ala Arg
485 490 495

Glu Gly Asn Leu Pro Leu Leu Ile Ala Pro Ala Leu Ala Ala Val
500 505 510

Leu Leu Ala Ala Leu Ala Ala Val Gly Ala Ala Tyr Cys Val Arg
515 520 525

Arg Gly Arg Ala Met Ala Ala Ala Ala Gln Asp Lys Gly Gln Val
530 535 540

Gly Pro Gly Ala Gly Pro Leu Glu Leu Glu Gly Val Lys Val Pro
545 550 555

Leu Glu Pro Gly Pro Lys Ala Thr Glu Gly Gly Glu Ala Leu
560 565 570

Pro Ser Gly Ser Glu Cys Glu Val Pro Leu Met Gly Phe Pro Gly
575 580 585

Pro Gly Leu Gln Ser Pro Leu His Ala Lys Pro Tyr Ile
590 595

<210> 70
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 70
ccctccactg cccccacggac tg 22

<210> 71
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 71
cggttctggg gacgttaggg ctcg 24

<210> 72
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 72
ctgccccaccg tccacactgcc tcaat 25

<210> 73
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 73
aggactgcc accgtccacc tgcctcaatg gggcacatg ccacc 45

<210> 74
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 74
acgcaaagcc ctacatctaa gccagagaga gacagggcag ctggg 45

<210> 75
<211> 1077
<212> DNA
<213> Homo Sapien

<400> 75
ggcacttagga caaccttctt cccttctgca ccactgccc 50
cgccccgcca cctccttgct accccactct tgaaaccaca gctgttgca 100
gggtccccag ctcatgccag cctcatctcc tttcttgcta gccccaaag 150
ggcctccagg caacatgggg ggcccagtca gagagccggc actctcagtt 200
gccctctggt tgagttgggg ggcagctctg ggggccgtgg cttgtgccat 250
ggctctgctg acccaacaaa cagagctgca gagcctcagg agagaggtga 300
gccggctgca ggggacagga ggccccctccc agaatggga agggtatccc 350
tggcagagtc tcccgagca gagttccgat gccctggaag cctggagaa 400

TO THE

tggggagaga tcccgaaaaa ggagagcagt gtcacccaa aaacagaaga 450
agcagcactc tgtcctgcac ctggttcca ttaacgccac ctccaaggat 500
gactccgatg tgacagaggt gatgtggcaa ccagctcta ggcgtggag 550
aggcctacag gcccaaggat atggtgtccg aatccaggat gctggagttt 600
atctgctgta tagccaggc tcgtttcaag acgtgacttt caccatgggt 650
caggtggtgt ctcgagaagg ccaaggaagg caggagactc tattccgatg 700
tataagaagt atgcctccc acccgaccc ggcctacaac agctgctata 750
gcgcaggtgt cttccattta caccaagggg atattctgag tgtcataatt 800
ccccgggcaa gggcgaaact taacctctct ccacatggaa ctttcctggg 850
gtttgtgaaa ctgtgattgt gttataaaaaa gtggctccc gcttgaaaga 900
ccaggggtggg tacatactgg agacagccaa gagctgagta tataaaggag 950
agggaatgtg caggaacaga ggcattttcc tgggtttggc tccccgttcc 1000
tcactttcc ctttcattc ccacccctta gactttgatt ttacggatat 1050
cttgcttctg ttccccatgg agctccg 1077

<210> 76
<211> 250
<212> PRT
<213> Homo Sapien

<400> 76
Met Pro Ala Ser Ser Pro Phe Leu Leu Ala Pro Lys Gly Pro Pro
1 5 10 15
Gly Asn Met Gly Gly Pro Val Arg Glu Pro Ala Leu Ser Val Ala
20 25 30
Leu Trp Leu Ser Trp Gly Ala Ala Leu Gly Ala Val Ala Cys Ala
35 40 45
Met Ala Leu Leu Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg
50 55 60
Glu Val Ser Arg Leu Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly
65 70 75
Glu Gly Tyr Pro Trp Gln Ser Leu Pro Glu Gln Ser Ser Asp Ala
80 85 90
Leu Glu Ala Trp Glu Asn Gly Glu Arg Ser Arg Lys Arg Arg Ala
95 100 105
Val Leu Thr Gln Lys Gln Lys His Ser Val Leu His Leu
110 115 120

BIOINFORMATICS

Val Pro Ile Asn Ala Thr Ser Lys Asp Asp Ser Asp Val Thr Glu
125 130 135
Val Met Trp Gln Pro Ala Leu Arg Arg Gly Arg Gly Leu Gln Ala
140 145 150
Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala Gly Val Tyr Leu Leu
155 160 165
Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe Thr Met Gly Gln
170 175 180
Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr Leu Phe Arg
185 190 195
Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr Asn Ser
200 205 210
Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile Leu
215 220 225
Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro
230 235 240
His Gly Thr Phe Leu Gly Phe Val Lys Leu
245 250
<210> 77
<211> 2849
<212> DNA
<213> Homo Sapien

<400> 77
cactttctcc ctctcttcct ttactttcga gaaaccgcgc ttccgcttct 50
ggtcgcagag acctcggaga ccgcgcgggg gagacggagg tgctgtgggt 100
gggggggacc tgtggctgct cgtaccgcgc cccaccctcc tcttctgcac 150
tgccgtcctc cggaagacct ttccccctgc tctgtttct tcaccgagtc 200
tgtgcatcgc cccggacctg gccgggagga ggcttggccg gcgggagatg 250
ctctaggggc ggcgcgggag gagcggccgg cggacggag ggcccgccag 300
gaagatgggc tcccgtggac agggactctt gctggcgtac tgcctgctcc 350
ttgcctttgc ctctggcctg gtcctgagtc gtgtgccccca tgtccagggg 400
gaacagcagg agtgggaggg gactgaggag ctgccgtcgc ctccggacca 450
tgccgagagg gctgaagaac aacatgaaaa atacaggccc agtcaggacc 500
aggggctccc tgcttccgg tgcttgcgt gctgtgaccc cggtacccctcc 550
atgtacccgg cgaccgcgt gccccagatc aacatcacta tcttgaaaagg 600
ggagaagggt gaccgcggag atcgaggcct ccaaggaaaa tatggcaaaa 650

caggctcagc aggggccagg ggccacactg gacccaaagg gcagaaggc 700
tccatgggg cccctggga gcggtgcaag agccactacg ccgcctttc 750
ggtgggcccgg aagaagccca tgcacagcaa ccactactac cagacggtga 800
tcctcgacac ggagttcgtg aacctctacg accacttcaa catgttcacc 850
ggcaagttct actgtacgt gccccccctc tacttcttca gcctaacct 900
gcacacctgg aaccagaagg agacctacct gcacatcatg aagaacgagg 950
aggaggtggt gatcttgttc ggcgcagggtgg ggcgcgcag catcatgcaa 1000
agccagagcc tgcgtggaa gctgcgagag caggaccagg tgtgggtacg 1050
cctctacaag ggcgaacgtg agaacgcatt cttcagcgag gagctggaca 1100
cctacatcac cttagtggc tacctggtca agcacgcac cgagccctag 1150
ctggccggcc acctccttcc ctctcgccac cttccacccc tgctgtgc 1200
tgaccccccacc gcctttcccc cgatccctgg actccgactc cctggctttg 1250
gcattcagtg agacgcctg cacacacaga aagccaaagc gatcggtgct 1300
cccagatccc gcagcctctg gagagagctg acggcagatg aaatcaccag 1350
ggcggggcac cggcgagaac cctctggac cttccgcggc cctctctgca 1400
cacatcctca agtgaccccg cacggcgaga cgcgggtggc ggcagggcgt 1450
cccagggtgc ggcaccgcgg ctccagtctt tggaaataat taggcaaatt 1500
ctaaaggctt caaaaggagc aaagtaaacc gtggaggaca aagaaaaggg 1550
ttgttatattt tgtctttcca gccagcctgc tggctccaa gagagaggcc 1600
tttcagttt agactctgct taagagaaga tccaaagtta aagctctggg 1650
gtcaggggag gggccggggg cagggaaacta cctctggctt aattcttta 1700
agccacgtag gaactttctt gagggatagg tggaccctga catccctgtg 1750
gccttgcucca agggctctgc tggctttctt gagtacagc tgctgggtga 1800
tggggctgg ggccccaggc gtcagcctcc cagagggaca gctgagcccc 1850
ctgccttggc tccaggttgg tagaagcagc cgaagggttc ctgacagtgg 1900
ccagggaccc ctgggtcccc caggcctgca gatgtttcta tgagggcag 1950
agctccttgg tacatccatg tgtggctctg ctccacccct gtgccacccc 2000
agagccctgg ggggtggctt ccatgcctgc caccctggca tcggctttct 2050
gtgccgcctc ccacacaaat cagccccaga aggccccggg gccttggctt 2100

TOP SECRET//COMINT

ctgttttta taaaacacct caagcagcac tgcaagtctcc catctccctcg 2150
tgggctaaggc atcaccgcctt ccacgtgtgt tgtgttggtt ggcagcaagg 2200
ctgatccaga ccccttctgc cccccactgcc ctcatccagg cctctgacca 2250
gtagcctgag aggggctttt tctaggcttc agagcagggg agagctggaa 2300
ggggctagaa agctcccgt tgcgtgtttc tcaggctctt gtgagcctca 2350
gtcctgagac cagagtcaag aggaagtaca cgtcccaatc acccgtgtca 2400
ggattcactc tcaggagctg ggtggcagga gaggcaatag cccctgtggc 2450
aattgcagga ccagctggag cagggttgcg gtgtctccac ggtgctctcg 2500
ccctgccccat ggccacccca gactctgatc tccaggaacc ccatagcccc 2550
tctccacccat accccatgtt gatgccagg gtcactcttg ctacccgctg 2600
ggcccccataa ccccccgtgc ctctcttctt tccccccatc ccccacctgg 2650
ttttgactaa tcctgcttcc ctctctggc ctggctgccc ggatctgggg 2700
tccttaagtc cctctttta aagaacttct gcgggtcaga ctctgaagcc 2750
gagttgctgt gggcgtgccc ggaagcagag cgccacactc gctgcttaag 2800
ctccccccagc tctttccaga aaacattaaa ctcagaattt tgtttcaa 2849

<210> 78

<211> 281

<212> PRT

<213> Homo Sapien

<400> 78

Met Gly Ser Arg Gly Gln Gly Leu Leu Leu Ala Tyr Cys Leu Leu
1 5 10 15

Leu Ala Phe Ala Ser Gly Leu Val Leu Ser Arg Val Pro His Val
20 25 30

Gln Gly Glu Gln Gln Glu Trp Glu Gly Thr Glu Glu Leu Pro Ser
35 40 45

Pro Pro Asp His Ala Glu Arg Ala Glu Glu Gln His Glu Lys Tyr
50 55 60

Arg Pro Ser Gln Asp Gln Gly Leu Pro Ala Ser Arg Cys Leu Arg
65 70 75

Cys Cys Asp Pro Gly Thr Ser Met Tyr Pro Ala Thr Ala Val Pro
80 85 90

Gln Ile Asn Ile Thr Ile Leu Lys Gly Glu Lys Gly Asp Arg Gly
95 100 105

Asp Arg Gly Leu Gln Gly Lys Tyr Gly Lys Thr Gly Ser Ala Gly

TOP SECRET - FEDERAL BUREAU OF INVESTIGATION

110

115

120

Ala Arg Gly His Thr Gly Pro Lys Gly Gln Lys Gly Ser Met Gly
125 130 135

Ala Pro Gly Glu Arg Cys Lys Ser His Tyr Ala Ala Phe Ser Val
140 145 150

Gly Arg Lys Lys Pro Met His Ser Asn His Tyr Tyr Gln Thr Val
155 160 165

Ile Phe Asp Thr Glu Phe Val Asn Leu Tyr Asp His Phe Asn Met
170 175 180

Phe Thr Gly Lys Phe Tyr Cys Tyr Val Pro Gly Leu Tyr Phe Phe
185 190 195

Ser Leu Asn Val His Thr Trp Asn Gln Lys Glu Thr Tyr Leu His
200 205 210

Ile Met Lys Asn Glu Glu Val Val Ile Leu Phe Ala Gln Val
215 220 225

Gly Asp Arg Ser Ile Met Gln Ser Gln Ser Leu Met Leu Glu Leu
230 235 240

Arg Glu Gln Asp Gln Val Trp Val Arg Leu Tyr Lys Gly Glu Arg
245 250 255

Glu Asn Ala Ile Phe Ser Glu Glu Leu Asp Thr Tyr Ile Thr Phe
260 265 270

Ser Gly Tyr Leu Val Lys His Ala Thr Glu Pro
275 280

<210> 79

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 79

tacaggccca gtcaggacca gggg 24

<210> 80

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 80

ctgaagaagt agaggccggg cacg 24

<210> 81

TOP SECRET//COMINT

<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 81
cccggtgctt gcgctgctgt gacccggta cctccatgta cccgg 45

<210> 82
<211> 2284
<212> DNA
<213> Homo Sapien

<400> 82
gcggagcata cgctcggtc ctcgcccaga ccccccgcgcg gattcgccgg 50
tccttccgc gggcgcgaca gagctgtcct cgcacctgga tggcagcagg 100
ggcgccccgg tcctctcgac gccagagaga aatctcatca tctgtgcagc 150
cttcttaaag caaactaaga ccagagggag gattatcctt gacccttgaa 200
gacaaaact aaactgaaat taaaaatgtt cttcgaaaaa gaagggagct 250
tgacttacac tttgtaata atttgcttcc tgacactaag gctgtctgct 300
agtcagaatt gcctcaaaaaa gagtctagaa gatgttgtca ttgacatcca 350
gtcatctctt tctaaggaa tcagaggcaa tgagccccgt aatacttcaa 400
ctcaagaaga ctgcattaat tcttgctgtt caacaaaaaa catatcaggg 450
gacaaaagcat gtaacttgat gatcttcgac actcgaaaaa cagctagaca 500
acccaactgc tacctatTT tctgtcccaa cgaggaagcc tgtccattga 550
aaccagcaaa aggacttatg agttacagga taattacaga ttttccatct 600
ttgaccagaa atttgccaag ccaagagta ccccaaggaag attctctctt 650
acatggccaa tttcacaag cagtcactcc cctagcccat catcacacag 700
attattcaaa gcccaccgat atctcatgga gagacacact ttctcagaag 750
tttggatcct cagatcacct ggagaaaacta tttaagatgg atgaagcaag 800
tgcccagctc cttgcttata aggaaaaagg ccattctcag agttcacaat 850
tttcctctga tcaagaaata gctcatctgc tgcctgaaaa tgtgagtgcg 900
ctccccagcta cggtggcagt tgcttctcca cataccacct cggctactcc 950
aaagccccgc acccttctac ccaccaatgc ttcagtgaca cttctggga 1000
cttcccagcc acagctggcc accacagctc cacctgtaac cactgtcaact 1050

DNA sequence analysis

tctcagcctc ccacgaccct catttctaca gttttcacac gggctgcggc 1100
tacactccaa gcaatggcta caacagcagt tctgactacc acctttcagg 1150
cacctacgga ctcgaaaggc agcttagaaa ccataccgtt tacagaaatc 1200
tccaacttaa ctttgaacac aggaaatgtg tataacccta ctgcactttc 1250
tatgtcaaat gtggagtctt ccactatgaa taaaactgct tcctggaaag 1300
gtagggaggc cagtccaggc agttcctccc agggcagtgt tccagaaaat 1350
cagtacggcc ttccatTTGA aaaatggctt cttatcgggt ccctgcttt 1400
tggtgtcctg ttccTGGTGA taggcctcgt ctcctgggt agaattcctt 1450
cggaatcact ccgcaggaaa cgTTactcaa gactggatta tttgatcaat 1500
gggatctatg tggacatcta aggatggaac tcgggtctc ttaattcatt 1550
tagtaaccag aagccaaat gcaatgagtt tctgctgact tgctagtcTT 1600
agcaggaggt tgtatTTGA agacaggaaa atgccccctt ctgctttcct 1650
ttttttttt ggagacagag tcttgctctg ttgcccaaggc tggagtgcag 1700
tagcacgatc tcggctctca ccgcaacotc cgttcctgg gttcaagcga 1750
ttctcctgcc tcagcctct aagtatctgg gattacaggc atgtgccacc 1800
acacctgggt gatTTTGTa ttttagtag agacggggTT tcaccatgtt 1850
ggtcaggctg gtctcaaact cctgacctag tgatccaccc tcctcgccct 1900
cccaaagtgc tgggattaca ggcattgagcc accacagctg gcccccttct 1950
gttttatgtt tggtttGTa gaaggaatga agtgggaacc aaatttaggtA 2000
atTTTGGGTa atctgtctct aaaatattag ctaaaaacaa agctctatgt 2050
aaagtaataa agtataattg ccatataaat ttcaaaattc aactggcttt 2100
tatgcaaaga aacaggttag gacatctagg ttccaaattca ttcacattct 2150
tggttccaga taaaatcaac tgTTtatATC aatttctaatt ggatttgctt 2200
ttcttttat atggattcct taaaaactta ttccagatgt agttccttcc 2250
aattaaatat ttgaataaaat cttttgttac tcaa 2284

<210> 83
<211> 431
<212> PRT
<213> Homo Sapien

<400> 83
Met Phe Phe Gly Gly Glu Gly Ser Leu Thr Tyr Thr Leu Val Ile
1 5 10 15

DRAFT

Ile Cys Phe Leu Thr Leu Arg Leu Ser Ala Ser Gln Asn Cys Leu
20 25 30
Lys Lys Ser Leu Glu Asp Val Val Ile Asp Ile Gln Ser Ser Leu
35 40 45
Ser Lys Gly Ile Arg Gly Asn Glu Pro Val Tyr Thr Ser Thr Gln
50 55 60
Glu Asp Cys Ile Asn Ser Cys Cys Ser Thr Lys Asn Ile Ser Gly
65 70 75
Asp Lys Ala Cys Asn Leu Met Ile Phe Asp Thr Arg Lys Thr Ala
80 85 90
Arg Gln Pro Asn Cys Tyr Leu Phe Phe Cys Pro Asn Glu Glu Ala
95 100 105
Cys Pro Leu Lys Pro Ala Lys Gly Leu Met Ser Tyr Arg Ile Ile
110 115 120
Thr Asp Phe Pro Ser Leu Thr Arg Asn Leu Pro Ser Gln Glu Leu
125 130 135
Pro Gln Glu Asp Ser Leu Leu His Gly Gln Phe Ser Gln Ala Val
140 145 150
Thr Pro Leu Ala His His Thr Asp Tyr Ser Lys Pro Thr Asp
155 160 165
Ile Ser Trp Arg Asp Thr Leu Ser Gln Lys Phe Gly Ser Ser Asp
170 175 180
His Leu Glu Lys Leu Phe Lys Met Asp Glu Ala Ser Ala Gln Leu
185 190 195
Leu Ala Tyr Lys Glu Lys Gly His Ser Gln Ser Ser Gln Phe Ser
200 205 210
Ser Asp Gln Glu Ile Ala His Leu Leu Pro Glu Asn Val Ser Ala
215 220 225
Leu Pro Ala Thr Val Ala Val Ala Ser Pro His Thr Thr Ser Ala
230 235 240
Thr Pro Lys Pro Ala Thr Leu Leu Pro Thr Asn Ala Ser Val Thr
245 250 255
Pro Ser Gly Thr Ser Gln Pro Gln Leu Ala Thr Thr Ala Pro Pro
260 265 270
Val Thr Thr Val Thr Ser Gln Pro Pro Thr Thr Leu Ile Ser Thr
275 280 285
Val Phe Thr Arg Ala Ala Ala Thr Leu Gln Ala Met Ala Thr Thr
290 295 300
Ala Val Leu Thr Thr Phe Gln Ala Pro Thr Asp Ser Lys Gly

TOP SECRET//COMINT

305

310

315

Ser Leu Glu Thr Ile Pro Phe Thr Glu Ile Ser Asn Leu Thr Leu
320 325 330

Asn Thr Gly Asn Val Tyr Asn Pro Thr Ala Leu Ser Met Ser Asn
335 340 345

Val Glu Ser Ser Thr Met Asn Lys Thr Ala Ser Trp Glu Gly Arg
350 355 360

Glu Ala Ser Pro Gly Ser Ser Ser Gln Gly Ser Val Pro Glu Asn
365 370 375

Gln Tyr Gly Leu Pro Phe Glu Lys Trp Leu Leu Ile Gly Ser Leu
380 385 390

Leu Phe Gly Val Leu Phe Leu Val Ile Gly Leu Val Leu Leu Gly
395 400 405

Arg Ile Leu Ser Glu Ser Leu Arg Arg Lys Arg Tyr Ser Arg Leu
410 415 420

Asp Tyr Leu Ile Asn Gly Ile Tyr Val Asp Ile
425 430

<210> 84

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 84

agggaggatt atccttgacc tttgaagacc 30

<210> 85

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 85

gaagcaagtg cccagctc 18

<210> 86

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 86

cgggtccctg ctctttgg 18

ESTABLISHED

<210> 87
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 87
caccgttagct gggagcgcac tcac 24

<210> 88
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 88
agtgttaagtc aagctcccc 18

<210> 89
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 89
gcttcctgac actaaggctg tctgcttagtc agaattgcct caaaaagag 49

<210> 90
<211> 957
<212> DNA
<213> Homo Sapien

<400> 90
cctggaagat gcgccattt gctggggcc tgctcaaggt ggtgttcgtg 50
gtcttcgcct ctttgtgtgc ctggatttcg gggtacctgc tcgcagagct 100
cattccagat gcaccctgt ccagtgctgc ctatagcatc cgccatcg 150
gggagaggcc tgcctcaaa gctccagtc cccaaaggca aaaatgtgac 200
cactggactc cctgcccattc tgacacctat gcctacaggt tactcagcgg 250
aggtggcaga agcaagtacg cccaaatctg ctttgaggat aacctactta 300
tgggagaaca gctggaaat gttgccagag gaataaacat tgccattgtc 350
aactatgtaa ctggaaatgt gacagcaaca cgatgtttt atatgtatga 400
aggcgataac tctggaccga tgacaaagtt tattcagagt gctgctccaa 450
aatccctgct cttcatggtg acctatgacg acgaaagcac aagactgaat 500

aacgatgcc aagaatccat agaagcac tt ggaagtaa ag aaatcaggaa 550
catgaaattc aggtctagct gggtatttat tgca gcaaaa ggcttggAAC 600
tcccttccga aattcagaga gaaaagatca accactctga tgctaagaac 650
aacagatatt ctggctggcc tgcagagatc cagatagaag gctgcataacc 700
caaagaacga agctgacact gcagggtcct gagtaaatgt gttctgtata 750
aacaaatgca gctggaatcg ctcaagaatc ttatTTTCT aaatccaaca 800
gccccatattt gatgagtatt ttgggtttgt tgtaaaccAA tgaacatTTG 850
ctagttgtat caaatcttgg tacgcagtat tttatacca gtatTTATG 900
tagtgaagat gtcaatttagc aggaaactaa aatgaatggA aattcttaaa 950
aaaaaaaa 957

<210> 91
<211> 235
<212> PRT
<213> Homo Sapien

<400> 91
Met Arg Pro Leu Ala Gly Gly Leu Leu Lys Val Val Phe Val Val
1 5 10 15
Phe Ala Ser Leu Cys Ala Trp Tyr Ser Gly Tyr Leu Leu Ala Glu
20 25 30
Leu Ile Pro Asp Ala Pro Leu Ser Ser Ala Ala Tyr Ser Ile Arg
35 40 45
Ser Ile Gly Glu Arg Pro Val Leu Lys Ala Pro Val Pro Lys Arg
50 55 60
Gln Lys Cys Asp His Trp Thr Pro Cys Pro Ser Asp Thr Tyr Ala
65 70 75
Tyr Arg Leu Leu Ser Gly Gly Arg Ser Lys Tyr Ala Lys Ile
80 85 90
Cys Phe Glu Asp Asn Leu Leu Met Gly Glu Gln Leu Gly Asn Val
95 100 105
Ala Arg Gly Ile Asn Ile Ala Ile Val Asn Tyr Val Thr Gly Asn
110 115 120
Val Thr Ala Thr Arg Cys Phe Asp Met Tyr Glu Gly Asn Ser
125 130 135
Gly Pro Met Thr Lys Phe Ile Gln Ser Ala Ala Pro Lys Ser Leu
140 145 150
Leu Phe Met Val Thr Tyr Asp Asp Gly Ser Thr Arg Leu Asn Asn
155 160 165

Asp Ala Lys Asn Ala Ile Glu Ala Leu Gly Ser Lys Glu Ile Arg
170 175 180

Asn Met Lys Phe Arg Ser Ser Trp Val Phe Ile Ala Ala Lys Gly
185 190 195

Leu Glu Leu Pro Ser Glu Ile Gln Arg Glu Lys Ile Asn His Ser
200 205 210

Asp Ala Lys Asn Asn Arg Tyr Ser Gly Trp Pro Ala Glu Ile Gln
215 220 225

Ile Glu Gly Cys Ile Pro Lys Glu Arg Ser
230 235

<210> 92

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 92

aatgtgacca ctggactccc 20

<210> 93

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 93

aggcttggaa ctcccttc 18

<210> 94

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 94

aagatttttg agcgattcca gctg 24

<210> 95

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 95

aatccctgct cttcatggtg acctatgacg acggaagcac aagactg 47

<210> 96
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 96
ctcaagaagc acgcgtactg c 21

<210> 97
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 97
ccaacacctag cttccgcctc tacga 25

<210> 98
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 98
catccaggct cgccactg 18

<210> 99
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 99
tggcaaggaa tggaaacagt 20

<210> 100
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 100
atgctgccag acctgatcgc agaca 25

<210> 101
<211> 19
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 101
gggcagaaat ccagccact 19

<210> 102
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 102
cccttcgcct gcttttga 18

<210> 103
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 103
gccatctaattgaagccat cttccca 27

<210> 104
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 104
ctggcggtgt ccttcctt 19

<210> 105
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 105
cctcgggtctc ctcatctgtg a 21

<210> 106
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

SEARCHED
INDEXED
FILED
SERIALIZED
FILED
INDEXED
SEARCHED
FILED
SERIALIZED

<223> Synthetic oligonucleotide probe

<400> 106

tggcccagct gacgagccct 20

<210> 107

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 107

ctcataggca ctcggttctg g 21

<210> 108

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 108

tggctccag cttggaaga 19

<210> 109

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 109

cagctttgg ctgtctccag tatgtaccca 30

<210> 110

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 110

gatgcctctg ttcctgcaca t 21

<210> 111

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 111

PROBE SEQUENCES

ggattctaat acgactcaact atagggctgc ccgcaacccc ttcaactg 48

<210> 112

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 112

ctatgaaatt aaccctcaact aaagggaccg cagctgggtg accgtgta 48

<210> 113

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 113

ggattctaat acgactcaact atagggccgc cccgccacct cct 43

<210> 114

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 114

ctatgaaatt aaccctcaact aaagggactc gagacaccac ctgaccac 48

<210> 115

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 115

ggattctaat acgactcaact atagggccca aggaaggcag gagactct 48

<210> 116

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide probe

<400> 116

ctatgaaatt aaccctcaact aaagggacta ggggtggga atgaaaag 48

<210> 117

TOE" "THE 60

<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 117
ggattctaat acgactcact atagggcccc cctgagctct cccgtgta 48

<210> 118
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 118
ctatgaaatt aaccctcact aaagggaagg ctcgccactg gtcgtaga 48

<210> 119
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 119
ggattctaat acgactcact atagggcaag gagccgggac ccaggaga 48

<210> 120
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 120
ctatgaaatt aaccctcact aaagggaggg ggcccttggt gctgagt 47